

**STIC-Biotech/ChemLib**

**67938**

**From:** Bunner, Bridget  
**Sent:** Tuesday, June 04, 2002 8:47 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** sequence search

Hi! I'd like the following sequence searched for case 09/655,272:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

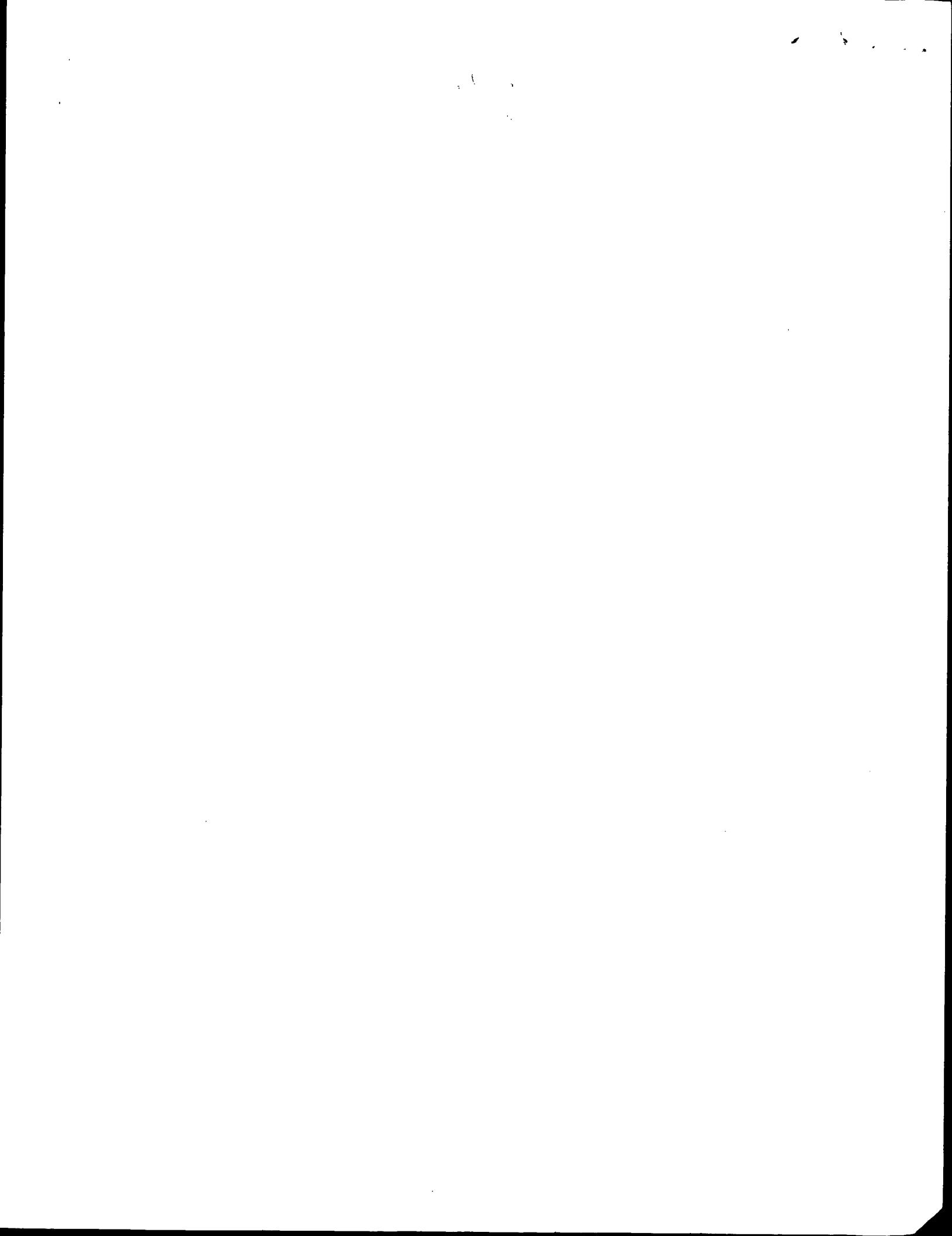
*Art Unit 1647  
CM1-10D12  
(703) 305-7148  
mailroom 10C01*

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 6/4/02  
Date Completed: 6/4/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: Q2  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_





DR InterPro; IPR003280; 2poreK channel.  
 DR InttPro; IPR000636; Cation-chan\_non\_lig.  
 DR InterPro; IPR001622; Channel\_pore\_K.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRO1333; 2POREKCHANNEL.  
 KW Glycoprotein; Alternative splicing; Ion transport; Potassium transport;  
 DOMAIN TRANSMEM 1 3  
 FT DOMAIN 89 24  
 FT TRANSMEM 119 139  
 FT DOMAIN 140 171  
 FT TRANSMEM 192 192  
 FT DOMAIN 222 222  
 FT TRANSMEM 235 255  
 FT DOMAIN 256 398  
 FT CARBOHYD 81 81  
 FT VARSPPLIC 63 67  
 FT VARSPLIC 68 398  
 SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AE0C2 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 2079; DB 1; Length 398;  
 Matches 398; Conservative 100.0%; Pred. No. 3.5e-105; RT  
 QY 1 MRSTTLLALLALVALYLIVSGALVQALEPHQHQAOAKMDHGRQFLRDPHPCVSQSL60  
 Db 1 MRSTTLLALLALVALYLIVSGALVQALEPHQHQAOAKMDHGRQFLRDPHPCVSQSL60  
 QY . 61 FKLIVEALGGGANPETSWNNSHSAWNLSGSAFFSGTTITIGGNTVLTAGRLF 120  
 Db 61 FKLIVEALGGGANPETSWNNSHSAWNLSGSAFFSGTTITIGGNTVLTAGRLF 120  
 QY 121 CFYALVGIFPLFGMLLAGYGDRIQSSERRGCHIEAFLKWHVPPGLVRSLSAVFLLIG 180  
 Db i21 CFYALVGIFPLFGMLLAGYGDRIQSSERRGCHIEAFLKWHVPPGLVRSLSAVFLLIG 180  
 QY 181 CLLFVLTPTPFVFSYMEWSKLAIRYFVITLTGQDGTVPGDGTQNSPAVPLWVWI 240  
 Db 181 CLLFVLTPTPFVFSYMEWSKLAIRYFVITLTGQDGTVPGDGTQNSPAVPLWVWI 240  
 QY 241 LEGFLAYAFASVLTIGNWLRAVSRTRAEAGLITQAASWGTPTARVQTORTESSPEK 300  
 Db 241 LEGFLAYAFASVLTIGNWLRAVSRTRAEAGLITQAASWGTPTARVQTORTESSPEK 300  
 QY 301 EQLPLPSLAPPAPAVVEPAGRGSPAPKVPESPPTPASALDPSENLAFTEDESDTOS 360  
 Db 301 EQLPLPSLAPPAPAVVEPAGRGSPAPKVPESPPTPASALDPSENLAFTEDESDTOS 360  
 QY 361 ERGCALPAPRGRRRPNSKKPSPRPGRLRKAVPV 398  
 Db 361 ERGCALPAPRGRRRPNSKKPSPRPGRLRKAVPV 398

RESULT 2  
 CIWA\_HUMAN  
 ID CIWA\_HUMAN  
 AC Q9NG8B;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Stimulated potassium channel subfamily K member 4 (TWIK-related arachidonic acid-  
 DE GN OR TRAAK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RC TISSUE=Brain;

DR InterPro; IPR003280; 2poreK channel.  
 DR InttPro; IPR000636; Cation-chan\_non\_lig.  
 DR InterPro; IPR001622; Channel\_pore\_K.  
 DR PRO1333; 2POREKCHANNEL.  
 KW Glycoprotein; Alternative splicing; Ion transport; Potassium transport;  
 DOMAIN TRANSMEM 1 3  
 FT DOMAIN 89 24  
 FT TRANSMEM 119 139  
 FT DOMAIN 140 171  
 FT TRANSMEM 192 192  
 FT DOMAIN 222 222  
 FT TRANSMEM 235 255  
 FT DOMAIN 256 398  
 FT CARBOHYD 81 81  
 FT VARSPPLIC 63 67  
 FT VARSPLIC 68 398  
 SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AE0C2 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 2079; DB 1; Length 398;  
 Matches 398; Conservative 100.0%; Pred. No. 3.5e-105; RT  
 QY 1 MRSTTLLALLALVALYLIVSGALVQALEPHQHQAOAKMDHGRQFLRDPHPCVSQSL60  
 Db 1 MRSTTLLALLALVALYLIVSGALVQALEPHQHQAOAKMDHGRQFLRDPHPCVSQSL60  
 QY . 61 FKLIVEALGGGANPETSWNNSHSAWNLSGSAFFSGTTITIGGNTVLTAGRLF 120

RX MEDLINE=20499203; PubMed=11042359;  
 RA Chapman C.G.; Meadows H.J.; Goddein R.J.; Campbell D.A.; Duckworth M.;  
 RA Kelsell R.E.; Murdock P.R.; Randall A.D.; Reinlie G.I.; Gloger I.S.;  
 RA cerebellum specific, two pore domain potassium channel.;  
 RA Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RT [2]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Frontal cortex;  
 RA Gray A.T.;  
 RT "Assignment of KCN4 encoding the human potassium channel TRAAK to  
 RL chromosome 11." Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP Sequence FROM N.A.  
 RX MEDLINE=2031639; PubMed=10767409;  
 RA Lesage F.; Mangivet F.; Lazdunski M.;  
 RT "Cloning and characterization of human TRAAK, a polyunsaturated fatty  
 acids-activated and mechano-sensitive K(+) channel.";  
 RT FBS Lett. 47:137-140(2000);  
 CC -I- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING  
 CC POTASSIUM CHANNEL, OUTWARD RECTIFICATION IS REVERSED AT HIGH  
 CC EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).  
 CC -I- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC CHANNELS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC modification and this statement is as long as its content is in no way  
 CC or send an email to license@lsb.sib.ch).  
 DR EMBL; AF248242; AAG31731; 1;  
 DR EMBL; AF247042; AAF64062; 1; ALT\_INTR.  
 DR MIM: 605720; -  
 DR InterPro; IPR03280; 2poreK\_channel.  
 DR InterPro; IPR00536; Cation Chanl\_pore\_K.  
 DR InterPro; IPR01632; Channel\_pore\_K.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR ICONE; PR02168; Occludin; 1.  
 DR KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 3  
 FT TRANSMEM 4 24  
 FT DOMAIN 89 113  
 FT TRANSMEM 118 138  
 FT DOMAIN 140 171  
 FT TRANSMEM 172 192  
 FT DOMAIN 197 221  
 FT TRANSMEM 234 254  
 FT DOMAIN 255 393  
 FT TRANSMEM 78 78  
 FT CARBOHYD 82 82  
 FT CONFLICT 328 328  
 SQ SEQUENCE 398 AA; 42704 MW; 7F1E53A0A94D57D CRC64;

Query Match  
 Best Local Similarity 81.4%; Score 1692.5; DB 1; Length 393;  
 Matches 328; Conservative 24; Mismatches 41; Indels 5; Gaps 2;  
 QY 1 MRSTTLLALLALVALYLIVSGALVQALEPHQHQAOAKMDHGRQFLRDPHPCVSQSL60  
 Db 1 MRSTTLLALLALVALYLIVSGALVQALEPHQHQAOAKMDHGRQFLRDPHPCVSQSL60  
 QY . 61 FKLIVEALGGGANPETSWNNSHSAWNLSGSAFFSGTTITIGGNTVLTAGRLF 120

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 CC  
 CC  
 EMBL; API19695; AAF75132.1; -  
 DR InterPro; IPR003280; 2poreK-channel.  
 DR InterPro; IPR00536; Cation\_chan\_non-lig.  
 DR InterPro; IPR001622; Channel\_pore\_K.  
 PRIM; PR00520; ion\_trans; 1.  
 DR PRINTS; PR01333; 2POREKCHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 FT Glycoprotein.  
 FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 72 92 POTENTIAL.  
 FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 182 202 POTENTIAL.  
 FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 234 254 POTENTIAL.  
 FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 299 319 POTENTIAL.  
 FT DOMAIN 320 358 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0A52B97E4 CRC64;

Query Match 37.9%; Score 788; DB 1; Length 538;  
 Best Local Similarity 51.9%; Pred. No. 8.1e-36;  
 Matches 152; Conservative 54; Mismatches 81; Indels 6; Gaps 3;

QY 1 MRSTILLALIALVLYLVSGALVFOALQALEPHQDQAOKKMDHGRDQFLRDHPCVSOKSLED 60  
 Db 67 MKWKWVVALEFWVVVVVLYLGIVLPGVRALEQPFPESQSKNTIALEKAFLRHDIVCYSPELET 126  
 QY 61 FIKLIVEALGGGANETSWNTNSNHSSAKNLGSAFFESTGTTITRIGVGNIVITDAGLF 120  
 Db 127 LIOHALDADNAGVSPV--GNNSNSSSHNDLGSAAFFAGTAVITIGVGNIAPISTEKKIF 183  
 QY 121 CIFYALVNGTIPLGMLLAGVGDRGSSLRGIGHIAEFLKWHPPGLYRLSLSVLFLIG 180  
 Db 184 CLVIAKFGPLPFLGLAGIDGDLGIFTGKSIARVEVKFRKKVQSQTKEVIRVISTILEFLAG 243  
 QY 181 CLFELVLTPTFVEVSMEWSKLEAYFVILTVTGFDGYPPGIGTGN-SPAYQLWFW 239  
 Db 244 CIVFTVTPAVIKEYIEGWTALESIVFWVWLTFVGFGDFVAGSGNAGNTYREWKPLWFW 303  
 QY 240 ILFGLAYFAVSLTIGNMURAVSRTRAMEGGTAOAASWTGTWTA-RVTOR 290  
 Db 304 ILVGLAYFAVLVLSMGDWLRVLSKTKBEVGEKAHAEWKANVAFRETTR 356

RESULT 5  
 CTW2\_MOUSE STANDARD: PRT; 411 AA.

FT TRANSMEM 47 67 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 129 155 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT DOMAIN 178 207 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 228 POTENTIAL.  
 FT DOMAIN 239 268 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 273 293 POTENTIAL.  
 FT DOMAIN 294 411 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 378 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY.  
 DE REQUIRED FOR BASAL CHANNEL ACTIVITY.  
 DE channel protein TREK-1 (Two-pore potassium channel TPCK1) (TREK-1 K+ channel subunit).  
 DE KCNK2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10909;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE-BRAIN:  
 RX MEDLINE-97157476; PubMed=2003761;

Query Match 37.1%; Score 770.5; DB 1; Length 411;  
 Best Local Similarity 49.8%; Pred. No. 5.4e-35;  
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;

QY 1 MRSTILLALIALVLYLVSGALVFOALQALEPHQDQAOKKMDHGRDQFLRDHPCVSOKSLED 60

RN [2]  
 RP REVISONS.  
 RC TISSUE-Brain;  
 RA Fink M.; Duprat F., Lesage F., Reyes R., Romeo G., Heurteaux C., Lazdunski M.;  
 RT "Cloning, functional expression and brain localization of a novel unconventional outward rectifier K<sup>+</sup> channel.";  
 RT EMBO J. 15:6854-6862(1996).  
 RL [3]  
 RP ACTIVATION.  
 RX MEDLINE-99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romeo G., Lazdunski M.;  
 RT "Inhalational anesthetics activate two-pore-domain background K<sup>+</sup> channels";  
 RL Nat. Neurosci. 2:422-426(1999).  
 CC -|- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -|- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -|- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN LIVER, IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB, HIPPOCAMPUS AND CEREBELLUM.  
 CC -|- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.  
 CC -|- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
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 CC ---  
 DR EMBL; U73488; AAC53005.2; -  
 DR MGI; 10336; Kenk2.  
 DR InterPro; IPR00280; 2poreK\_channel.  
 DR InterPro; IPR00636; Cation\_chan\_non\_lig.  
 DR InterPro; IPR01622; Channel\_pore\_K.  
 DR InterPro; IPR003976; Trek\_channel.  
 PRIM; PR00520; ion\_trans; 1.  
 DR PRINTS; PR01333; 2POREKCHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 FT Glycoprotein.  
 FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 47 67 PORE-FORMING 1 (POTENTIAL).  
 FT DOMAIN 129 155 POTENTIAL.  
 FT TRANSMEM 157 177 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 178 207 POTENTIAL.  
 FT TRANSMEM 238 228 PORE-FORMING 2 (POTENTIAL).  
 FT DOMAIN 239 268 POTENTIAL.  
 FT TRANSMEM 273 293 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 294 411 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY.  
 DE REQUIRED FOR BASAL CHANNEL ACTIVITY.  
 DE channel protein TREK-1 (Two-pore potassium channel TPCK1) (TREK-1 K+ channel subunit).  
 DE KCNK2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10909;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE-BRAIN:  
 RX MEDLINE-97157476; PubMed=2003761;

Db 42 MKWKTIVSTIFLWVVLJIGAAFKALEQPOEISQRTTIVIQKQFIAQHACVNTELDE 101  
 QY 61 FIKLIVEALGGGANPETSWNNSNHSSAWNLSAFLFGSGTITIGYGNVLHTDAGLF 120  
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 102 LIQQIVAAINAGIIP--LGNSNQVSHWDLGSFFAGTIVITIGFGNISPRTEGGKIF 158  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 121 CIFVALVGIPFLGMLLAGVUGRLGSSLRGIGHIEAITLKWHVPPGLVRSIAVFLIG 180  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 159 CITYALGIPFLGFLLAGVGDQLTIFGKGIAKVEDTIFKWNVSQTKIRISTIFILFG 218  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 181 CLFVLTPPFVFVFSMESHWSKLEAIFYVIVLTVGFGDYPGDDGTQNSPAVQPLWFWI 240  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 219 CVLFVALPAVIFKHESWAIDAVIVWVITTTIGFQYVAGGSDEIYLDFYKPVWFWI 273  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 241 LFGLAYFASVLTIGNWLRAVSRRTRAENGGLTAQASWTGVTVA 285  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 279 LVGLAYFAVLSMIGRLRVISKTKKEEVGEFRAHAETANVTA 323  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 6  
 CIW2\_HUMAN STANDARD; PRT; 426 AA.

ID CIW2\_HUMAN STANDARD; PRT; 426 AA.  
 AC 095069; 09UNE3;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore potassium channel TPCK1).  
 DE KCNK2 OR TRK1 OR TREK.  
 OS Homo sapiens (Human).  
 OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Roney G., Lazdunski M.;  
 RT "Inhalational anaesthetics activate two-pore-domain background K+ channels.";  
 RL Nat. Neurosci. 2:422-426(1999).  
 RN [2]  
 SEQUENCE FROM N.A.  
 TISSUE=Brain;  
 RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -!- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, HALOTHANE AND ISOFURANE.  
 CC -!- SIMILARITY: BELONGS TO THE TWO-PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
 CC -----  
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 CC -----  
 DR EMBL; AFI2399; AAD47569.1; --.  
 DR EMBL; AF00471; AAD01203.1; --.  
 DR InterPro; IPR00280; 2poreK\_channel.  
 DR InterPro; IPR00636; Cation\_channnon\_lig.  
 DR InterPro; IPR00162; Channel\_pore\_K.  
 DR InterPro; IPR00376; Trek\_channel.  
 DR Pfam; PF00520; Ion\_trans\_1.  
 DR PRINTS; PRO133; 2POREKCHANNEL.  
 DR PRINTS; PRO1499; TREKCHANNEL.  
 DR Ionic\_channel; transmembrane; Ion\_transport; Potassium\_transport;

KW GLYCOPROTEIN.  
 FT DOMAIN 1 61  
 FT TRANSMEM 62 82  
 FT DOMAIN 144 170  
 FT TRANSMEM 172 192  
 FT DOMAIN 193 223  
 FT TRANSMEM 224 244  
 FT DOMAIN 253 283  
 FT TRANSMEM 288 308  
 FT DOMAIN 309 426  
 FT DOMAIN 378 426  
 FT DOMAIN 354 426  
 FT CARBOHYD 110 110  
 FT CARBOHYD 134 134  
 FT CONFLICT 2 16  
 FT CONFLICT 309 311  
 FT CONFLICT 391 391  
 FT CONFLICT 411 411  
 SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;

Query Match Best Local Similarity 36.5%; Score 759.5; DB 1; Length 426; Matches 140; Conservative 57; Mismatches 85; Indels 3; Gaps 1; Db 57 MKWKTIVSTIFLWVVLJIGAAFKALEQPOEISQRTTIVIQKQFIAQHACVNTELDE 116  
 QY 61 FIKLIVEALGGGANPETSWNNSNHSSAWNLSAFLFGSGTITIGYGNVLHTDAGLF 120  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 117 LIQQIVAAINAGIIP--LGNTSNQVSHWDLGSFFAGTIVITIGFGNISPRTEGGKIF 173  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 QY 121 CIFVALVGIPFLGMLLAGVUGRLGSSLRGIGHIEAITLKWHVPPGLVRSIAVFLIG 180  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 174 CITYALGIPFLGFLLAGVGDQLTIFGKGIAKVEDTIFKWNVSQTKIRISTIFILFG 233  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 QY 181 CLFVLTPPFVFVFSMESHWSKLEAIFYVIVLTVGFGDYPGDDGTQNSPAVQPLWFWI 240  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 234 CVLFVALPAVIFKHESWAIDAVIVWVITTTIGFQYVAGGSDEIYLDFYKPVWFWI 273  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 QY 241 LFGLAYFASVLTIGNWLRAVSRRTRAENGGLTAQASWTGVTVA 285  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 294 LVGLAYFAVLSMIGRLRVISKTKKEEVGEFRAHAETANVTA 323  
 || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 7  
 CIW5\_HUMAN STANDARD; PRT; 499 AA.

ID CIW5\_HUMAN STANDARD; PRT; 499 AA.  
 AC 095079;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Potassium channel subfamily K member 5 (acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).  
 DE KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 SEQUENCE FROM N.A.  
 TISSUE=Kidney;  
 MEDLINE=9903043; PubMed=9812978;  
 RX Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,  
 RA Lazdunski M.;  
 RT "Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney";  
 J. Biol. Chem. 273:30863-30869 (1998).  
 CC -!- FUNCTION: PH-gated, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL

CC K+ CONCENTRATIONS.  
 CC -!- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED  
 CC IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION  
 CC IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT  
 CC EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 -!- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL  
 AC ACIDIFICATION.  
 CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.

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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial/  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).

CC EMBL; AR084830; AAC79458 1; -  
 DR MIM; 603493; -  
 DR InterPro; IPR003200; ZporeK.channel.  
 DR InterPro; IPR00656; Cation chan non\_1qg.  
 DR InterPro; IPR01622; Channel\_pore\_K.  
 DR Print; PR00520; ion\_trans; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 8 25 POTENTIAL.  
 FT DOMAIN 85 112 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 180 POTENTIAL.  
 FT DOMAIN 190 215 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.  
 FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 499 AA; 55130 MW; E871A7N4823DDA00 CRC64;

Query Match 20.0%; Score 416; DB 1; Length 499;  
 Best Local Similarity 27.6%; Pred. No. 6.7e-16; Matches 115; Conservative 66; Mismatches 139; Indels 96; Gaps 14;

QY 9 LIAALVLYLVSGALVFOALEQPFREQQAKKMDHQGRDFQLRDPVCVSQKSLEDPIKLVEA 68  
 Db 8 LTTSAIIYLFLAIGAIIFEVLEEPHKWKEAKKNVYIQLHLIKEFFCLGQBGLDKLILEVNSDA 67

QY 69 LGGGGANPETSWTNNSNHSSAWNNGSAFFFSGTITTYGYGNVLTHTDAGRLFCIFYALVG 128  
 Db 68 AGCG---VATIQNQTFNM-WNPWNAMFAATTIVITTYGYGNVAPKTPTAGRFLCFVFGF 122

QY 129 IPR-----FGMLLAGYDRGSSL-RRGIGHIAEFLKWHPPGLVRSLSAVLFLLIG 180  
 Db 123 VPCPLTWISALGKFFGGRAKRLQFLTKRGVSRLKA-----QITCIVIFIWG 170

QY 181 CILFVLPTPFVMSMESMSKLEIYIVFVLTIVGFDGVPGCTGQNSPA YQPLVFW 239  
 Db 171 VLHLVLPFVFENAVTEGNYIEGLYSITISTIGEGLFVAGVNPSANYHALYRYFELW 230

QY 240 IIFGLAYFASVLTITGNWL-----RAVSRETRA----ENGLGLAQAASTGTVA- 285  
 Db 231 IVGLAW----LSLFVNWKVSKMVEVHKARRRRKESFESSPHSKRKLQVKGSTASK 286

QY 286 -----RVTQET-----GPSAPPPEKEOPPLESSPAPPA 314  
 Db 287 DNTIFSLSKKEETYNDLIKQIKKAMKTSGGGTGPGPGLGPGQGGIPALPDSL-VPL 344

QY 315 WVPAGRGSPAPAEKVETPSPTASADYPSRNLAFIGDESSQTSERGCALERAP 370

Db 345 WWSKRN-----VPTLEEVQSOTLRSKGHVRSRPDEE----AVARAP 381

RESULT 8  
 CIW6\_HUMAN STANDARD; PRT; 313 AA.  
 ID CIW6\_HUMAN STANDARD; PRT; 313 AA.  
 AC Q9Y257; O9HBA47; -  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Potassium channel subfamily K member 6 (inward rectifying potassium  
 DE channel protein TWIK-2) (TWIK-originated similarity sequence).  
 GN KCNE6 OR TWIK2 OR TOSS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] R P SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=restis; PubMed=10359073;  
 RX MEDLINE=99283568; PubMed=10075682;  
 RA Pountney D.J., Guikarov I., Vega-Saenz de Miera E., Holmes D.,  
 RA Saenzich M., Rudy B., Artman M., Goetzee W.A.; "Identification and cloning of TWIK-originated similarity sequence  
 RT "TWIK-2, a novel human 2-pore K+ channel principal subunit";  
 RL FEBS Lett. 450:191-196(1999).  
 RN [2] R P SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CYS-53.  
 RC TISSUE=Brain; PubMed=10075682;  
 RX MEDLINE=99175662; PubMed=10075682;  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RA Mehta Y., Forssayeth J.R., Yost C.S.; "TWIK-2, a new weak inward rectifying member of the tandem pore domain  
 RT potassium channel family";  
 RL J. Biol. Chem. 274:7887-7892(1999).  
 RN [3] R P ERRATUM.  
 RA Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,  
 RA Mehta Y., Forssayeth J.R., Yost C.S.; "TWIK-2, an inactivating 2P domain K+ channel";  
 RL J. Biol. Chem. 275:28722-28730(2000).  
 J. Biol. Chem. 275:28722-28730(2000).  
 -!- FUNCTION: Exhibits outward rectification in a physiological K(+) gradient and mild inward rectification in symmetrical K(+) conditions.  
 CC -!- SUBUNIT: HOMODIMER (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN PLACENTA, PANCREAS, HEART, COLON AND SPLEEN. LOWER LEVELS DETECTED IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.  
 CC -!- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDINE OR BARIUM.  
 CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF134149; AAD29901; -  
 DR EMBL; AF117708; AAD240001; -.



QY	61	FIKLIVELAAGGG---ANPETSWNNSNHSSAWNLGSAFFSGIITTTIGIGNVILHTDA	116	CC	or send an email to license@isb-sib.ch.
Db	78	FLGRVIEASNYGVSVISNASGNW-----WDT; S1 : I:::    :::  :  :  :	129	CC	-
DR	EMBL; AF033017; AACI61973; 1;	DR	MGI; MGID: 105322; Kcnk1.		
DR	INTERPRO; IPR005280; 2poreK_channel.	DR	INTERPRO; IPR005636; Cation_chann_non_lig.		
DR	INTERPRO; IPR005636; Cation_chann_non_lig.	DR	INTERPRO; IPR005636; Channel_Pore_K.		
DR	INTERPRO; IPR005636; Channel_Pore_K.	DR	INTERPRO; IPR005636; Twik1_channel.		
DR	INTERPRO; IPR005636; Twik1_channel.	DR	PRINTS; PROJ133; 2POREKCHAN.		
DR	PRINTS; PROJ133; 2POREKCHAN.	DR	KW		
QY	232	YQPLWFWLFLGLAYFASVLT	253	KW	Ionic channel; Transmembrane; Ion transport; Potassium transport;
Db	245	YKIGTCYLLGLITMLVVL	266	FT	Glycoprotein, 1
OS	MUS musculus (Mouse).	FT	DOMAIN	20	CYTOPLASMIC (POTENTIAL).
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;	FT	TRANSMEM	21	POTENTIAL.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	FT	PORE	41	PORE FORMING 1 (POTENTIAL).
NCBI_TaxID=10090;	[1]	FT	TRANSMEM	104	POTENTIAL.
RC	SEQUENCE FROM N.A.	FT	DOMAIN	130	POTENTIAL.
RC	[2]	FT	TRANSMEM	133	POTENTIAL.
RC	STRAIN FROM N.A.	FT	DOMAIN	153	CYTOSPLASMIC (POTENTIAL).
RC	Lesage F., Lauritzen T., Duprat F., Reyes R., Fink M., Heurteaux C.,	FT	TRANSMEM	154	POTENTIAL.
RC	Lazdunski M., "The structure, function and distribution of the mouse TWIK-1 K <sup>+</sup> channel.", FEBS Lett. 402:28-32(1997).	FT	DOMAIN	178	POTENTIAL.
RC	Arrigoni T., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;	FT	TRANSMEM	212	PORE FORMING 2 (POTENTIAL).
RC	"Structure, chromosome localization, and tissue distribution of the mouse twik K <sup>+</sup> channel gene.";	FT	DOMAIN	247	POTENTIAL.
RC	FEBS Lett. 425:310-316(1998).	FT	TRANSMEM	268	CYTOSPLASMIC (POTENTIAL).
RC	-- SUBUNIT: HOMODIMER (POTENTIAL).	FT	CARBOHYD	95	N-LINKED (GLCNAc. .) (POTENTIAL).
RC	-- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN, KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE, EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELTAL MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL CORTEX.	FT	SEQUENCE	336 AA;	A996060A18266FD4 CRC44;
RC	-- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND STABILIZES AFTER DAY 8.	FT	Query	Match	Query Match
RC	-- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL ACTIVATION ACTIVATED BY PROTEIN KINASE C.	Db	Best Local Similarity	17.8%; Score 369.5;	Best Local Similarity
RC	-- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.	Db	Matches	DB 1; length 336;	Matches
RC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	Db	Indels	34.0%; Pred No. 1.4e-13;	Indels
RC		Db	Gaps	53; Mismatches	Gaps
RC		Db	QY	2 RSTTILLALIAL-VVLYLVSGLYFOALEQFPHSQAQKKMDHORDELDRHDHCVSOKSLEDLRLRKRLRFLERHEECLSEPOEQ 77	QY
RC		Db	QY	61 FIKLIVELAAGGG---ANPETSWNNSNHSSAWNLGSAFFSGIITTTIGIGNVILHTDA	116
RC		Db	QY	176 -FLIGGCLFLVLTPTFWFSYME-SWSKLEAIYFVLTITVFGDYVPGDGTON-SPA	231
RC		Db	QY	232 YQPLWFWLFLGLAYFASVLT	253
RC		Db	QY	245 YKIGTCYLLGLITMLVVL	266
RC		RESULT	11	FT	SEQUENCE FROM N.A.
RC		OR1_DROME		FT	TISSUE=Larva;
RC		OR1_DROME		FT	MEDLINE=97075152; PubMed=8917578;
RC		STANDARD;		FT	GOlistStein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.;
RC		PT		FT	"OR1", a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster by expression in Saccharomyces



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CC  
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CC  
DR EMBL; AF212827; AAF63706.1; -.  
DR InterPro; IPR003280; SporeK.channel.  
DR InterPro; IPR006345; Cation\_chan\_non\_lig.  
DR InterPro; IPR001622; Channel\_pore\_K.  
DR InterPro; IPR003092; TASK.channel.  
DR Pfam; PF00520; ion\_trans\_1.  
DR Prints; PRO1333; 2POREKCHANNEL.  
DR Prints; PRO1095; TASKCHANNEL.  
DR KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
GW Glycoprotein.  
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 9 29 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 78 101 PORE-FORMING 1 (POTENTIAL).  
FT DOMAIN 108 128 POTENTIAL.  
FT TRANSMEM 129 158 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 159 179 POTENTIAL.  
FT TRANSMEM 184 207 PORE-FORMING 2 (POTENTIAL).  
FT DOMAIN 219 239 POTENTIAL.  
FT CARBOHD 240 365 CYTOPLASMIC (POTENTIAL).  
SQ SEQUENCE 53 365 N-LINKED (GlcNAc . .) (POTENTIAL).  
SQ SEQUENCE 365 AA; 40769 MW; -261DC97FF53AF91 CRC64;

Query Match 16.0%; Score 333.5; DB 1; Length 365;  
Best local Similarity 28.3%; Pred. No. 1 3e-11; Indels 85; Gaps 12; Matches 104; Conservative 55; Mismatches 124; RT "Proton block and voltage gating are potassium-dependent in the cardiac leak channel Kcnk3.",  
Oy 7 LALIALVLYLVSGAVALQFOALEQPHQCAQKMMHDGRDQFLRDPVCYSQK--SLEDFIK 63 CC  
Db 9 LSILACIPTYTYLWGAFAVDAEESDHEEREEL--KAER--IRGKNNISTEDYRQ 61 CC  
Oy 64 LIVEALGGGANPETSWTNSSNHSA - WNLGSAFFSGTITITIGCNIVLHTDAGRIFC 121 CC  
Db 62 LEIVLIL-----QSEPHRAGYKWFAGSFYVATIVITITIGHAACTDGAKFC 110 CC  
Oy 122 IFYALVGIPLRFLMLLAGVGDRGLRGSSLRGIGHIEATFLKWHVPPGLVRSLSAVFLLIGC 181 CC  
Db 111 MFYAVLGIPITWFMQSLIGERANTFVYLKRIKKCGMRNTEEVSMENMVTFGFFSCMT 170 CC  
Oy 182 LLFVLTPTEFVSYMEWSKLRAFYVFLTUVGFQDYV - PGDGTCQNSPAVQPLWFW 239 CC  
Db 171 LCII--GAATASSQCEEMSSFFHAYYCCITLTGFGQYVALQSKGALQRKPPVYAFSMY 227 CC  
Oy 240 ILFLGLAYF-----ASVLTIGNWRARVSRTR 266 CC  
Db 228 ILVGLTVIGAFLNLVVLRLFLTMNSDEERGEGBEGAALPGPNPSSVVTHISEBARQRYR 287 CC  
Oy 267 AEMGGLTQAQASWTTGTVTARYVQRTGFS -----APPE----KEOPLPLLSSL----P 310 CC  
Db 288 GEGGDQI-----SVSCACYRSQPNFGATLAPOPLHSISCREEISSTLKNLFP 339 CC  
Oy 311 APPAVVEP 318 CC  
Db 340 SPISIISVP 347 CC  
  
RESULT 13  
ID CIW3\_MOUSE STANDARD; PRT; 409 AA.  
AC 035111; 035163; 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K<sup>+</sup> channel)  
DE (Cardiac two-pore background K<sup>+</sup> channel) (CTBAK-1).  
GN KUNK3 OR TASK OR CTBAK.  
  
OS musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI-TAXID=10090;  
RN [1];  
RP SOURCE FROM N.A.  
RP TISSUE=Heart;  
RX MEDLINE=98165556; PubMed=10748056;  
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;  
RA Kim D., Fujita A., Horio Y., Kurachi Y.;  
RT Cloning and functional expression of a novel cardiac two-pore background K<sup>+</sup> channel (CTBAK-1).";  
RT background K<sup>+</sup> channel (CTBAK-1).";  
RN Circ. Res. 82:513-518(1998);  
RN [2];  
RP TISSUE=Heart;  
RX MEDLINE=20287574; PubMed=10748056;  
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;  
RA J. Biol. Chem. 275:16969-16978 (2000).  
RN [3];  
RP SEQUENCE OF 4-409 FROM N.A.  
RX MEDLINE=9743932; PubMed=9312005;  
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
RA EMBJ 16:5464-5471(1997).  
CC FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM CHANNEL CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW (BY SIMILARITY).  
CC SUBUNIT: HOMODIMER (POTENTIAL).  
CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC TISSUE SPECIFICITY: Very strong expression in heart, also detected in kidney, brain, skin, testis, lung, skeletal muscle, small intestine and stomach. Not detected in liver, thymus or spleen.  
CC INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.  
CC MISCELLANEOUS: INACTIVATED BY BARTUM.  
CC SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.  
  
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DR EMBL; AB008537; BAA25436.1; -.  
DR EMBL; AF241798; AAF81418.1; -.  
DR EMBL; AF42508; AAF81418.1; JOINED.  
DR EMBL; AF065162; AAG29339.1; -.  
DR EMBL; AF00624; AAC53367.1; -.  
DR EMBL; AB013345; BAA20349.1; -.  
DR MGII; MGII:1100509; Kcnk3.  
DR Prints; PRO1333; 2POREKCHANNEL.  
DR Prints; PRO1095; TASKCHANNEL.  
DR Prints; PRO1622; Channel\_pore\_K.  
DR InterPro; IPR003092; TASK.channel.  
DR InterPro; IPR00336; Cation\_chan\_non\_lig.  
DR InterPro; IPR00330; SporeK.channel.  
DR InterPro; IPR00333; 2POREKCHANNEL.  
DR KW Glycoprotein.  
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 9 29 PORE-FORMING 1 (POTENTIAL).  
FT DOMAIN 78 101 POTENTIAL.  
FT TRANSMEM 108 128 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 129 158 POTENTIAL.  
FT TRANSMEM 159 179 PORE-FORMING 2 (POTENTIAL).  
FT DOMAIN 184 207 CYTOPLASMIC (POTENTIAL).  
FT CARBOHD 240 365 CYTOPLASMIC (POTENTIAL).  
SQ SEQUENCE 53 365 N-LINKED (GlcNAc . .) (POTENTIAL).  
SQ SEQUENCE 365 AA; 40769 MW; -261DC97FF53AF91 CRC64;

FT TRANSMEM 223 243 POTENTIAL. (POTENTIAL).  
 FT DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).  
 FT CARBONYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 4 4 Q -> E (IN REF. 3).  
 FT 123 V -> I (IN REF. 3).  
 SEQUENCE 409 AA; 45068 MW; 3523EB01AAC5607 CRC64;

Query Match 16.0%; Score 332.5; DB 1; Length 409;  
 Best Local Similarity 31.6%; Pred. No. 1.7e-11; Indels 43; Gaps 7;  
 Matches 85; Conservative 44; Mismatches 97; Gaps 43; Gaps 7;

QY 7 LALLALVLLIVYSGALVQALEQPHEQQAKKMDHGRDQFLRDHPCVSQNSLEDFIKLV 66  
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 9 LALIVCFTYLTVLGAFAVDALESEPERIQRLEL-ROLELRARYNLSSEGYYEELRV 67

QY 67 EALGGGANPETSWTNSSNNHSSAWNLGSAFFSGSTIITIGIGNVILHTDAGRIFCYAL 126  
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 68 RLKPHKAQVQ-----WRFAGSFYFAITVITIGGHAAFPSTDGGKVFCMFYAL 115

QY 127 VGPPLFGMLLAGVGDRIGSSLR-----RGIG--HIEATFLKWHVPPGLYRLSAVLFL 177  
 :|||: :|||: :|||: :|||: :|||: :|||: :|||:  
 Db 116 LGIPLTLVMFOSLGERINTFVYLLHRAKRGLGMRAE-----VSMANMVLIG 163

QY 178 LIGCLLFVLTPTVFVFSMEWSKLEAFVIVLTLTGVGFDDV--PGDGTCGONSPAYQPL 235  
 :|||: :|||: :|||: :|||: :|||: :|||:  
 Db 164 FVSCISTICGAAFFSYERWFQAOYCYCTLTIGFGDYVALQKDQALQTQPOY-- 220

QY 236 VWFWILEGLAYFASVLTIGNWLRASRR 264  
 |||: |||: |||: |||: |||: |||:  
 Db 221 ---VAFSFWVLTIGLTVIGAFLNLVLR 245

RESULT 14  
 ID CIW3\_RAT STANDARD: PRT: 411 AA.  
 AC 054912;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K<sup>+</sup> channel).  
 GN KCNK3 OR TASK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammal; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TAXID=10116;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=cerebellum;  
 RX MEDLINE=98097979; PubMed=9437008;  
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor B.M., Chavez R.A., Forszeth J.R., Yost C.S.;  
 RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum".  
 RL J. Neurosci. 18:868-877(1998).

FT PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).  
 --!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 --!- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.  
 --!- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUTYRICACID AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.  
 CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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 CC DR EMBL; AF031384; AAC39952.1; -  
 CC DR InterPro; IPRO03280; sporek\_channel.  
 CC DR InterPro; IPRO0636; Cation\_chan\_non\_lig.  
 CC DR InterPro; IPRO1622; Channel\_Pore\_K.  
 CC DR InterPro; IPRO03092; TASK\_channel.  
 CC DR Pfam; PF00520; ion\_trans\_1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTER; PRO1095; TASKCHANNEL.  
 KW Glycoprotein.  
 FT DOMAIN 1 8  
 FT TRANSMEM 9 29  
 FT DOMAIN 78 101  
 FT TRANSMEM 108 128  
 FT DOMAIN 129 158  
 FT TRANSMEM 159 179  
 FT DOMAIN 184 207  
 FT TRANSMEM 223 243  
 FT DOMAIN 244 411  
 FT CARBONYD 53 53  
 SEQUENCE 411 AA; 45276 MW; D2778016902BF5 CRC64;

Query Match 16.0%; Score 332.5; DB 1; Length 411;  
 Best Local Similarity 31.6%; Pred. No. 1.7e-11; Indels 43; Gaps 7;  
 Matches 85; Conservative 44; Mismatches 97; Gaps 43; Gaps 7;

QY 7 LALLALVLLIVYSGALVQALEQPHEQQAKKMDHGRDQFLRDHPCVSQNSLEDFIKLV 66  
 |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 9 LALIVCFTYLTVLGAFAVDALESEPERIQRLEL-ROLELRARYNLSSEGYYEELRV 67

QY 67 EALGGGANPETSWTNSSNNHSSAWNLGSAFFSGSTIITIGIGNVILHTDAGRIFCYAL 126  
 |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 68 RLKPHKAGVQ-----WRFAGSFYFAITVITIGGHAAFPSTDGGKVFCMFYAL 115

QY 127 VGPPLFGMLLAGVGDRIGSSLR-----RGIG--HIEATFLKWHVPPGLYRLSAVLFL 177  
 :|||: :|||: :|||: :|||: :|||: :|||:  
 Db 116 LGIPLTLVMFOSLGERINTFVYLLHRAKRGLGMRAE-----VSMANMVLIG 163

QY 178 LIGCLLFVLTPTVFVFSMEWSKLEAFVIVLTLTGVGFDDV--PGDGTCGONSPAYQPL 235  
 :|||: :|||: :|||: :|||: :|||:  
 Db 164 FVSCISTICGAAFFSYERWFQAOYCYCTLTIGFGDYVALQKDQALQTQPOY-- 220

QY 236 VWFWILEGLAYFASVLTIGNWLRASRR 264  
 |||: |||: |||: |||: |||:  
 Db 221 ---VAFSFWVLTIGLTVIGAFLNLVLR 245

RESULT 15  
 ID CIW9\_HUMAN STANDARD: PRT: 374 AA.  
 AC 09NP02;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K<sup>+</sup> channel 3).  
 GN KCNK9 OR TASK3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.  
 OX NCBI\_TAXID=9606;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RX MEDLINE=2087350; PubMed=10747866;  
 RA Reajan S., Wissmeyer E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Derst C.;

RT \*TASK-3, a novel tandem pore domain acid-sensitive K<sup>+</sup> channel. An extracellular histidine as pH sensor.;  
 RL J. Biol. Chem. 277:16650-16657(2002).  
 RN [2]  
 RP  
 RC  
 TISSUE-Cerebellum;  
 MEDLINE=20499203; PubMed=11042359;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,  
 RA Kelsell R.E., Murdoch P.R., Randall A.D., Rennie G.I., Glover I.S.;  
 RT \*Cloning, localisation and functional expression of a novel human,  
 RT cerebellum specific, two pore domain potassium channel.;;  
 RL Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Girard C., Lesage F., Tinel N., Lazdunski M.;  
 RA "Human Task-3, a novel 2P domain potassium channel related to Task.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Vega-Senz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,  
 RA Coetzee W., Rudy B.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.  
 CC -I- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM  
 CC CHANNEL PROTEIN.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -I- TISSUE SPECIFICITY: MAINLY FOUND IN THE CEREBELLUM.  
 CC -I- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM  
 CC CHANNELS.  
 CC  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announcements.html>) or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; AF212829; AAF63708.1; .  
 DR EMBL; AF248241; AAG31730.1; .  
 CC EMBL; AF299809; AAF85982.1; .  
 DR EMBL; AF250807; ARG33126.1; .  
 DR MIM; 605874; .  
 DR InterPro; IPR01280; 2POREK-channel.  
 DR InterPro; IPR00536; Cation\_channel\_lig.  
 DR InterPro; IPR01622; Channel\_pore\_K.  
 DR Pfam; PF0520; ion\_trans; 1.  
 DR PRINTS; PRO1333; 2POREKCHANNEL.  
 DR PRINTS; PRO1095; TASKCHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Potassium transport;  
 KW Glycoprotein.  
 FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 9 29 POTENTIAL.  
 FT DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 108 128 POTENTIAL.  
 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 219 239 POTENTIAL.  
 FT DOMAIN 240 374 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC . . .) (POTENTIAL).  
 SQ SEQUENCE 374 AA; 42263 MW; 8A199EE5A4D7F38 CRC64;  
 Query Match 15.8%; Score 327.5; DB 1; Length 374;  
 Best Local Similarity 28.7%; Precl. No. 2.9e-11; Gaps  
 Matches 107; Conservative 54; Mismatches 147; Indexes 65; Gaps  
 Matches 107; Conservative 54; Mismatches 147; Indexes 65; Gaps  
 QY 7 LALLALVLLVLYSGALVFOQALEPHQHQOAKKMDHGRDQFLRDHPVCYSQK--SLEDFIK 63  
 QY |::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 9 LSLIVCTFTYLNGAAVDALESDHMREEKL--KAEIFR---IKGKYNNISSEDYRQ 61

Search completed: June 4, 2002, 11:03:40  
Job time: 204 sec

Tue Jun 4 11:44:25 2002

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 4, 2002, 10:56:40 ; Search time 31:63 Seconds  
 (without alignments)  
 (without alignments)  
 1397.641 Million cell updates/sec

Title: US-09-655-272-2

Perfect score: 1 MRSTTLALLALVLYLVSG. . . . . . SKKPSRPRGPGRRLRDKAVPV 398

Sequence:

Scoring table: BLOSUM62

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

1: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

2: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*

5: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*

6: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*

7: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*

8: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*

9: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:\*

10: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*

11: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

12: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

13: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*

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16: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:\*

17: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

18: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*

19: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*

20: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

21: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

22: /\$IDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	2079	100.0	398	AY30647 A mechanically sensitive potassium channel protein TRAK-1
2	1692.5	81.4	393	AY94425 Human h-TRAK poly
3	1692.5	81.4	393	AY94426 Human h-TRAK poly
4	1692.5	81.4	393	AKG6777 Human G-protein co
5	1688.5	81.2	1314	AKU04571 Human K channel TR
6	895	43.0	421	ABB12229 Human potassium ch
7	776.5	37.3	411	AY34133 h-TREK1 polypeptid
8	776.5	37.3	411	AY24496 Human TREK-1 potas
9	776.5	37.3	411	AKE10341 Human TREK-1
10	776.5	37.3	411	AIR5044 Homo mechanically sen
11	776.5	37.3	370	AY30648 A mechanically sen

**ALIGNMENTS**

12	770.5	37.1	411	20 AAY28497 Mouse h-TREK1 poly
13	770.5	37.1	411	21 AAE10342 Murine TREK-1 poly
14	759.5	36.5	426	22 AAU07618 Human potassium io
15	755.5	36.3	426	22 AAU07623 Human potassium io
16	754.5	36.3	426	22 AAU07624 Human potassium io
17	753.5	36.2	426	22 AAU07625 Human potassium io
18	751.5	36.1	332	21 AAY9054 Human TWIK-3 prote
19	427.5	20.6	332	22 AAE01027 Human TWIK-3 prote
20	427.5	20.6	499	21 AAY90556 Human TWIK-3 prote
21	416	20.0	499	21 AAY97675 Human potassium ch
22	416	20.0	499	21 AAY94875 Human protein clon
23	416	20.0	499	22 AAE01026 Human TWIK-2 prote
24	416	20.0	511	22 ABG26753 Novel human diagno
25	416	20.0	511	22 ABG26753 Novel human diagno
26	397.5	19.1	32	386 Human EST encoded
27	386	18.6	313	20 AAV34132 Human potassium ch
28	386	18.6	313	20 AAV25116 Human TWIK-1 prot
29	386	18.3	336	18 AAW23397 Human TWIK-1 prot
30	386	18.3	313	21 AAY9673 Human TWIK-4 prote
31	386	18.6	313	22 AAE01028 Human TWIK-4 prote
32	386	18.3	336	18 AAW23397 Human TWIK-4 prote
33	379.5	18.3	336	21 AAY9673 Novel human diagno
34	379.5	18.3	383	22 ABG0731 K74, a TWIK family
35	377.5	18.3	383	22 ABG0731 K75, a TWIK family
36	361.5	17.4	361	22 AAB31805 Drosophila melanog
37	353	17.0	107	20 ABB58298 Partial h-TREK1 po
38	343	16.5	405	21 AAY9673 Human TWIK-4 prote
39	332.5	16.0	374	21 AAY9673 Human TWIK-4 prote
40	327.5	15.8	374	21 AAB18813 Amino acid sequenc
41	327.5	15.8	374	22 AAB63938 Amino acid sequenc
42	327.5	15.8	374	22 AAE10343 Murine TASK potas
43	326.5	15.7	394	21 AAY79674 Human potassium ch
44	326.5	15.7	394	21 AAV87291 Human signal pepti
45	326.5	15.7	394	21 AAV87291 Human signal pepti

PT specific modulators, potential therapeutic agents for heart and nervous system disorders

XX

PS Claim 2; Fig 1; 40pp; French.

XX

CC The present sequence represents a mechanically sensitive potassium channel protein designated TRAK. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g., epilepsy, cardiovascular disease (arrhythmia), neurodegenerative (particularly where associated with ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases.

CC Antibodies specific for the protein are used to detect it in tissues, also as therapeutic inhibitors or activators.

CC

XX Sequence 398 AA;

PS

Query Match Best Local Similarity 100.0%; Score 2079; DB 20; Length 398; Matches 398; Conservative 0; Pred. No. 4e-169; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSTLLALLALVILLYVSGALVFOALEQPEDQOAKKMHGRDOFLRHPVCQSOKSLED 60

Db 1 mrstllallalvilyvsgalvfoaleqpedqoakkmhgrdoflrhpvcqsokslled 60

QY 61 FIKLVEALGGANPENSWTNTSSNSHSSAWNNGSAFFSGTTITIGKNIWHTDAGLF 120

Db 61 fiklvealgganpenswtntssnsawnnngsaaffsgttitigkniwhtdaglf 120

QY 121 CIFYALVGIPFGMLLAGVSRGKIGHTEAFLKWKWVPGIVRSISAVLFLIG 180

Db 121 cifyalvgipfgmllagvsrgrgkighteaflkwkvpgivrsisavlfiling 180

QY 181 CILFWVLTPTFESTMSWSKLEATIYVFLVLTIVFGDYVPGDTGCONSPAYQPLWFWI 240

Db 181 cilfvltpftfivsmevsksleatyvflvltivfgdyvpgdtgconspayqplwfwi 240

QY 241 LFLGLAFASVLTITGNWLRASVSRTRAMGGTAQASWGTWTRVTRGTPGSAPPER 300

Db 241 lfglayfasvlttgnwlrasvstrtramggtaqaswgtwtrvtrgtpgsapper 300

QY 301 EQPLIPSSSLAPPAPVWAGRGSPAPPAEKEVTPSPPTASALDOPSENLAFTEDSQTOS 360

Db 301 eqplipssslappapvwagrgspappaeketpspttasaldopsenlaftessqtos 360

QY 361 ERGCAALPAPRRRNPPSKPSRPGPGRKURDKAVPV 398

Db 361 ergcalpaprpprnpkpsrpgprkrirkavpv 398

---

RESULT 2

AY94425 ID AY94425 standard; Protein; 393 AA.

AC AY94425;

XX

DT 04-AUG-2000 (first entry)

DE Human h-TRAK polypeptide #1.

XX

KW Human; h-TRAK; potassium channel polypeptide;

KW 2P domain potassium channel; neurodegenerative disease; stroke;

KW psychiatric disorder; neurological disorder; Gene therapy;

OS Homo sapiens.

XX

PN WO200026253-A1.

XX 11-MAY-2000.

XX .

XX

PS

Query Match Best Local Similarity 100.0%; Score 2079; DB 20; Length 398; Matches 398; Conservative 0; Pred. No. 4e-169; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSTLLALLALVILLYVSGALVFOALEQPEDQOAKKMHGRDOFLRHPVCQSOKSLED 60

Db 1 mrstllallalvilyvsgalvfoaleqpedqoakkmhgrdoflrhpvcqsokslled 60

QY 61 FIKLVEALGGANPENSWTNTSSNSHSSAWNNGSAFFSGTTITIGKNIWHTDAGLF 120

Db 61 fiklvealgganpenswtntssnsawnnngsaaffsgttitigkniwhtdaglf 120

QY 121 CIFYALVGIPFGMLLAGVSRGKIGHTEAFLKWKWVPGIVRSISAVLFLIG 180

Db 121 cifyalvgipfgmllagvsrgrgkighteaflkwkvpgivrsisavlfiling 180

QY 181 CILFWVLTPTFESTMSWSKLEATIYVFLVLTIVFGDYVPGDTGCONSPAYQPLWFWI 240

Db 181 cilfvltpftfivsmevsksleatyvflvltivfgdyvpgdtgconspayqplwfwi 240

QY 241 LFLGLAFASVLTITGNWLRASVSRTRAMGGTAQASWGTWTRVTRGTPGSAPPER 300

Db 241 lfglayfasvlttgnwlrasvstrtramggtaqaswgtwtrvtrgtpgsapper 300

QY 301 EQPLIPSSSLAPPAPVWAGRGSPAPPAEKEVTPSPPTASALDOPSENLAFTEDSQTOS 360

Db 301 eqplipssslappapvwagrgspappaeketpspttasaldopsenlaftessqtos 360

QY 361 ERGCAALPAPRRRNPPSKPSRPGPGRKURDKAVPV 398

Db 361 ergcalpaprpprnpkpsrpgprkrirkavpv 398

---

RESULT 3

AY94426 ID AY94426 standard; Protein; 393 AA.

AC AY94426;

XX

us-09-655-272-2.rag

QY 61 FIKLVEALGGGANPETSWINNSNHSSAWNLGSAFFSGTITTCGYNTVHTDAGRLF 120  
 ||| : ||||: ||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 61 likevaldgipqgadpetnsnsh-sawnlgsaffsgtlttigvgnaltdagrif 119  
 XX  
 QY 121 CIFYALVGFLFGMLLAGVDRGSSLRGIGHTEAFLKMKHPPGSYRSLSAVELIG 180  
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 120 cifyalvgipqfpgillagydrigssrhgihieafikwhppelvrvsamfling 179  
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 QY 181 CLIVLTPPTFVFSYMEWSKSLAEIYFVITLTWGVGDYVPGDGRQNSAYQPLWFWI 240  
 |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 180 cilfvtpfvcymedwskleaiyfvitltvgdyyvagadbrqspayqlpwfi 239  
 |||: |||: |||: |||:  
 QY 241 LFLGLAYFASVLTIGNMRARVSRTRAEMGCTAQASWGTWAVTORTGPSAPPK 300  
 |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 240 llglayfasvlttignwlrvsrrtaemgtlaasawtgvttarvtqragaaappk 239  
 |||: |||:  
 QY 301 EQPLPSSLPAPPAVVEPAGPGSPAPAKEWVETSPPTASALDYPSENIAFPIDESDTOS 360  
 |||: |||: |||: |||: |||: |||: |||:  
 Db 300 epl---lpppcpaqp1grprspbsppkakqppspptasa1dypseniafpidesdtos 355  
 |||: |||:  
 QY 361 ERGCALPRAPIRGRGRNPNPSKPSRRRGPGRLDKAVP 398  
 |||: |||:  
 Db 356 ergcplpaprgrgrtrppkpvprgrprdkgvp 393  
 |||:  
 RESULT 5  
 AAU04571  
 ID AAU04571 standard; Protein; 1314 AA.  
 XX  
 AC AAU04571;  
 XX  
 DT 17-DEC-2001 (first entry)  
 DE Human G-protein coupled receptor like protein, GPCR #8.  
 KW Human; G-protein coupled receptor like protein; GPCR; immunogen;  
 KW ophthalmic disease; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; immunological disorder; HIV; candidiasis;  
 KW human immunodeficiency virus; autoimmune disorder; multiple sclerosis;  
 KW systemic lupus erythematosus; rheumatoid arthritis; platelet disorder;  
 KW thrombocytopenia; aplastic anaemia; inflammatory disorder;  
 KW septic shock; systemic inflammatory response syndrome; SIRS;  
 KW hormonal dysfunction; cancer; atherosclerosis; wound;  
 KW tissue regeneration; haemophilia; leukaemia; reperfusion injury;  
 KW psoriasis; diabetes; h-TAK4 polypeptide #1.  
 OS Homo sapiens.  
 XX  
 WO200153454-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 22-DEC-2000; 2000WO-US34983.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 20-JUN-2000; 2000US-059042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 31- AUG-2000; 2000US-0633450.  
 PR 04-DEC-2000; 2000US-0729739.  
 PA (HYSE-) HISEQ INC.  
 XX  
 PI Yamazaki V, Tang YT, Liu C, Zhou P, Wang D, Zhang J, Ren F;  
 XX  
 DR WPT; 2001-44225747.  
 DR N-PSDB; AAS08652.

New G-protein-coupled receptor-like polypeptides and polynucleotides, useful for treating diseases of ophthalmic, neurological, immunological and nephritic systems and hormonal dysfunction, cancer, atherosclerosis

XX  
 PS claim 10; Page 203-208; 259pp; English.  
 XX  
 CC The sequence represents a human G-protein coupled receptor (GPCR)-like protein, found to be homologous to human h-TAK4 polypeptide #1. The GPC-like polypeptides and polynucleotides are useful for the treatment of diseases of ophthalmic, neurological (e.g. Alzheimer's disease and Parkinson's disease, immunological (e.g. HIV infection and candidiasis), autoimmune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and rheumatoid arthritis), platelet disorders (e.g. thrombocytopaenia and aplastic anaemia), inflammatory disorders (e.g. septic shock and systemic inflammatory response syndrome, SIRS) and nonpruritic systems. They may also be used to treat hormonal dysfunction, cancer, atherosclerosis, wounds, tissue regeneration, haemophilia, leukemias, reperfusion injury, psoriasis and diabetes. Numerous examples of each type of disorder are given in the specification. Anti-GPCR-like protein antibodies are useful for detecting or quantitating the polypeptide in tissue. The polypeptides can also be used as molecular weight markers and as a food supplement.

Sequence 1314 AA;

Query Match Best Local Similarity 81.2%; Score 1688.5; DB 22; Length 1314; Matches 327; Conservative 82.4%; Pred. No. 3.7e-135; Mismatches 41; Index 5; Gaps 2;

QY 1 MRSSTLLALALAVLYLIVSGLVFOALEQPIEQQQAKMHDGRDFLDRHPCVSQSKLD 60  
 Db 540 mristllalalavlylvsgalvtraleqqpeqqsgregevrekftrahpcsdqeq1 599  
 QY 61 FIKLVEALGGGANPETSWINNSNHSSAWNLGSAFFSGTITTCGYNTVHTDAGRLF 120  
 Db 600 likevaldgipqgadpetnsnsh-sawnlgsaffsgtlttigvgnaltdagrif 658  
 QY 121 CIFYALVGFLFGMLLAGVDRGSSLRGIGHTEAFLKMKHPPGSYRSLSAVELIG 180  
 Db 659 cilfvtpfvcymedwskleaiyfvitltvgdyyvagadbrqspayqlpwfi 778  
 QY 181 CLIVLTPPTFVFSYMEWSKSLAEIYFVITLTWGVGDYVPGDGRQNSAYQPLWFWI 240  
 Db 719 cilfvtpfvcymedwskleaiyfvitltvgdyyvagadbrqspayqlpwfi 778  
 QY 241 LFLGLAYFASVLTIGNMRARVSRTRAEMGCTAQASWGTWAVTORTGPSAPPK 300  
 Db 779 llglayfasvlttignwlrvsrrtaemgtlaasawtgvttarvtqragaaappk 838  
 QY 301 EQPLPSSLPAPPAVVEPAGPGSPAPAKEWVETSPPTASALDYPSENIAFPIDESDTOS 360  
 Db 839 epl---lpppcpaqp1grprspbsppkakqppspptasa1dypseniafpidesdtos 894  
 QY 361 ERGCALPRAPIRGRGRNPNPSKPSRRRGPGRLDKAVP 398  
 Db 895 ergcplpaprgrgrtrppkpvprgrprdkgvp 931  
 RESULT 6  
 ABB12229  
 ID ABB12229 standard; peptide; 421 AA.  
 XX  
 AC ABB12229;  
 XX  
 DT 11-JAN-2002 (first entry)  
 XX  
 DE Human K channel TRAAK homologue, SEQ ID NO:2599.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor; hematopoiesis regulation; tissue growth; immunomodulator; activin; inhibitor; chemotaxis; chemokinesis; thrombolytic; oncogenesis; proliferation; metastasis; cancer; tumour; haemopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;

XX	KW	bone disorder; osteoporosis; vascular growth disorder;
XX	KW	tissue regeneration; wound healing; infection; immune disorder;
XX	KW	cell culture; drug screening; gene therapy; antiinflammatory;
XX	KW	antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
XX	KW	cytostatic; osteoprotective; vasotrophic; cardiotonic; virucide; antibacterial;
XX	KW	antifungal; vulnerary; antiulcer.
OS		Homo sapiens.
XX	PN	WO200151788-A2.
XX	PD	09-AUG-2001.
XX	PP	05-FEB-2001; 2001WO-US03800.
XX	PR	03-FEB-2000; 2000US-049914.
XX	PR	27-APR-2000; 2000US-0560875.
PA	(HYSE-) HYSEQ INC.	
XX	PI	Tang YT, Liu C, Drmanac RT;
XX	DR	WPI; 2001-457740/49.
XX	DR	N-PSPB; ABA09473.
PS		Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
PS		Claim 20; Page 318; 1963pp; English.
XX		Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA09225-ABA09374 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide or the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various biological activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth activity; haemopoiesis regulatory activity; activation- or inhibition-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorder (e.g., osteoporosis) and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
SQ	Sequence	4.21 AA;

CC cell types and biochemical pathways. Defective potassium channels are  
 CC known to cause four human diseases: episodic ataxia with myokymia;  
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.  
 CC As potassium channels are critical components of virtually all cells,  
 CC it is likely that abnormal potassium channels are also implicated in  
 CC certain renal, cardiovascular and central nervous system (CNS)  
 CC disorders. Nucleotides encoding K<sup>+</sup>Hvov proteins may be used for  
 CC identifying homologous or related proteins and the DNA sequences encoding  
 CC them. They may be used to produce compositions that modulate the  
 CC expression and function of the K<sup>+</sup>Hvov protein and in studying the  
 CC biochemical pathways associated with it. They may also be used for the  
 CC recombinant production of K<sup>+</sup>Hvov protein in fermentation cultures.  
 CC Additionally, such nucleotides may be used in gene therapy protocols for  
 CC the treatment of diseases associated with abnormal potassium channels.  
 XX Sequence 411 AA;

## SQ

Query Match 37.3%; Score 776.5; DB 20; Length 411;  
 Best Local Similarity 49.8%; Pred. No. 5.7e-58; XX  
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1; PT  
 QY 1 MRSTILLALVALVLYLVSGLALVFOALEQPHQQAQKMDHGRDOFLRDHPCVSOKSLED 60 PT  
 DB 42 mkwktvstifivvvlylqatvfkaleqpheisqrtrivqkqfqfisqscvnstelde 101 PT  
 QY 61 FIKLVEALGGGANPETSWINNSNHSAWNIGSAFFSGTITTTGYNLTVLHTDAGRLF 120 PT  
 DB 102 liqqivaainagip--lgnntsinqshwdlgsffagtttqgnisprteggkf 158 PT  
 QY 121 CIFVALVGIPFGLAGVRGSRLLRGIGHIAFLKWHVPPGLRSLSAVLFLLIG 180 PT  
 DB 159 ciyaligipifgfflagvqdqltgikqgiakvedtfikwnvsqtikristifilg 218 PT  
 QY 181 CLIFVLPPTFVSYMESWSKLEAIFTIVLTLTVGFDYVPGDGTCQNSPAYQPLWFWI 240 PT  
 DB 219 cvlfvalpaikfhiedwsaldaiyfvvtiltigfdytaggsdileydlykpvwwfwl 278 PT  
 QY 241 LFGLAYFASVINTIGNLRAVSRRAEMGLTAQQAASWWTGVTVA 285 PT  
 DB 279 lvglayfaavismigdwirviskkkeevegefrahaewtanvta 323 PT

## RESULT 8

AY28496

ID AAY28496 standard; Protein; 411 AA.

## XX

AC AAY28496;

DT 12-OCT-1999 (first entry)

DE h-TREK1 polypeptide.

XX

KW h-TREK1; two pore potassium channel; inflammatory disease;

XX

OS Homo sapiens.

XX

PN WO9337762-A1.

XX

PD 29-JUL-1999.

XX

PR 02-DEC-1998; 98WO-EP07805.

XX

PR 09-OCT-1998; 98GB-0022135.

PR 27-JAN-1998; 98EP-0300570.

(SMIK ) SMITHKLINE BEECHAM PLC.  
 Chapman CG, Meadows HJ;  
 XX WPI: 1999-469126/39.  
 DR N-PSDB; AAZ00039.

XX New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases  
 PT  
 XX Claim 3; Page 24; 44PP; English.

Query Match 37.3%; Score 776.5; DB 20; Length 411;  
 Best Local Similarity 49.8%; Pred. No. 5.7e-58; XX  
 Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1; PT  
 QY 1 MRSTILLALVALVLYLVSGLALVFOALEQPHQQAQKMDHGRDOFLRDHPCVSOKSLED 60 PT  
 DB 42 mkwktvstifivvvlylqatvfkaleqpheisqrtrivqkqfqfisqscvnstelde 101 PT  
 QY 61 FIKLVEALGGGANPETSWINNSNHSAWNIGSAFFSGTITTTGYNLTVLHTDAGRLF 120 PT  
 DB 102 liqqivaainagip--lgnntsinqshwdlgsffragtttqgnisprteggkf 158 PT  
 QY 121 CIFVALVGIPFGLAGVRGSRLLRGIGHIAFLKWHVPPGLRSLSAVLFLLIG 180 PT  
 DB 159 ciyaligipifgfflagvqdqltgikqgiakvedtfikwnvsqtikristifilg 218 PT  
 QY 181 CLIFVLPPTFVSYMESWSKLEAIFTIVLTLTVGFDYVPGDGTCQNSPAYQPLWFWI 240 PT  
 DB 219 cvlfvalpaikfhiedwsaldaiyfvvtiltigfdytaggsdileydlykpvwwfwl 278 PT  
 QY 241 LFGLAYFASVINTIGNLRAVSRRAEMGLTAQQAASWWTGVTVA 285 PT  
 DB 279 lvglayfaavismigdwirviskkkeevegefrahaewtanvta 323 PT

## RESULT 9

AAE10341

ID AAE10341 standard; Protein; 411 AA.

XX

AC AAE10341;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human TREK-1 potassium channel protein.

XX

KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;

XX

OS Homo sapiens.

XX

PN WO20004738-A2.

XX

PD 17-AUG-2000.

XX

PR 11-FEB-2000; 2000WO-1B00226.

XX

PR 12-FEB-1999; 99US-0119727.

XX

PR 11-FEB-2000; 2000US-0503089.

XX

(CNRS ) CNRS CENT NAT RECH SCI.

XX

PA Lazdunski M, Honore E, Lescage F, Romeo G, Patel AJ;

XX

PI



PD 10-SEP-1999.  
 XX  
 PF 23-FEB-1999; 99WO-FR00404.  
 XX  
 PR 05-MAR-1998; 98FR-0002725.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PT Honore E, Fink M, Lazzunski M, Lesage F, duprat F;  
 XX  
 DR WPI; 1999-551038/4-6.  
 DR N-PSDB; AAZ10607.  
 XX  
 PT New mechanically sensitive potassium channel, used to screen for  
 PT specific modulators, potential therapeutic agents for heart and nervous  
 PT system disorders -  
 XX  
 PS Claim 3; Page 23-25; 40pp; French.  
 CC The present sequence represents a mechanically sensitive potassium  
 CC channel protein designated TREK-1. The protein is activated by  
 CC polyunsaturated fatty acids, particularly arachidonic acid, and by  
 CC riluzole. The protein is used to screen for specific modulators which  
 CC are useful for treating or preventing diseases of the heart and nervous  
 CC systems in humans and animals, e.g. epilepsy, cardiovascular disease  
 CC (arrhythmia), neurodegeneration (particularly where associated with  
 CC ischemia or anoxia), abnormalities of hormone secretion and muscular  
 CC disease. The protein itself may be used to treat these diseases.  
 CC Antibodies specific for the protein are used to detect it in tissues,  
 CC also as therapeutic inhibitors or activators.  
 XX Sequence 370 AA;  
 SQ

Query Match 37.1%; Score 770.5; DB 20; Length 370;  
 Best Local Similarity 49.8%; Pred. No. 1.8e-57;  
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;  
 QY 1 MRSPTILLALATLVLYLIVSGALVFOALBOPHQCAQKKMDHGRDQFLRDHPCVSQKSLED 60  
 Db 42 mkkwtvstiflvwvlyiigaavkaleqpgeisqrtrivqktfiaqhaevnstele 101  
 QY 61 FIKLVLVERALGGGANPETSWTNNSNHSSAWNLSGSAFFSGTITITIGGNIVLHTDAGRF 120  
 Db 102 l1qqivaaanagip--lgnssnqvshwalgssffragtvttingfgnisprteggkf 158  
 QY 121 CTFYALVGIPLEGMLLAGVGDRGSSLRRGIGHIEAFLKWKWVPPGLVRSLSAVFLIG 180  
 Db 159 ciyaliglipqflagvgdqgtifgkiaekvdftikwnvsqtirkiristifilf 218  
 QY 181 CTFYALVGIPLEGMLLAGVGDRGSSLRRGIGHIEAFLKWKWVPPGLVRSLSAVFLIG 240  
 Db 219 cvlfvalpavifkhiedwsaldaiyfvitlttigfgyaggasdiedlfykpvwwfw 278  
 QY 241 LFGLAYFASVLTITGNMRRAVSRRTRAEMGLTAQAASWTGTVA 285  
 Db 279 lvglayfaavvismlgdwlrvisktkeevgefrahaewtanvta 323

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RESULT\_12  
 AAY28497  
 ID AAY28497 standard; Protein; 411 AA.  
 XX  
 AC AAY28497;  
 DT 12-OCT-1999 (first entry)  
 XX  
 DE Mouse h-TREK1 polypeptide.  
 XX  
 h-TREK1; two pore potassium channel; inflammatory disease;  
 KW chromosome 1q32.  
 XX  
 OS Mus musculus.

XX W09937762-A1.  
 PN  
 XX  
 PD 29-JUL-1999.  
 XX  
 PR 02-DEC-1998; 98WO-EP07805.  
 XX  
 PR 09-OCT-1998; 98GB-0022135.  
 PR 27-JAN-1998; 98EP-0300570.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Chapman CG, Meadows RJ;  
 XX  
 DR WPI; 1999-469126/39.  
 DR N-PSDB; AAZ00040.  
 XX  
 PT New two pore potassium channel used for, e.g. treatment of cancer,  
 PT pulmonary, cardiovascular and inflammatory diseases  
 XX  
 PS Claim 3; Page 26; 44pp; English.  
 CC This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
 CC poly nucleotide AAZ00040. h-TREK1 is a two pore potassium channel.  
 CC The poly nucleotide sequence of h-TREK1 can be used to diagnose a  
 CC disease or susceptibility to a disease related to expression or activity  
 CC of h-TREK1 polypeptides. The methods of diagnosis may be used in the  
 CC treatment of diseases including cancer, pulmonary, cardiovascular, and  
 CC inflammatory diseases, pain, psychiatric disorders including depression  
 CC and schizophrenia, neurodegenerative diseases including Alzheimer's,  
 CC stroke, and head trauma and neurological disorders including migraine.  
 XX  
 SQ Sequence 411 AA;

Query Match 37.1%; Score 770.5; DB 20; Length 411;  
 Best Local Similarity 49.8%; Pred. No. 1.8e-57;  
 Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;  
 QY 1 MRSPTILLALATLVLYLIVSGALVFOALBOPHQCAQKKMDHGRDQFLRDHPCVSQKSLED 60  
 Db 42 mkkwtvstiflvwvlyiigaavkaleqpgeisqrtrivqktfiaqhaevnstele 101  
 QY 61 FIKLVLVERALGGGANPETSWTNNSNHSSAWNLSGSAFFSGTITITIGGNIVLHTDAGRF 120  
 Db 102 l1qqivaaanagip--lgnssnqvshwalgssffragtvttingfgnisprteggkf 158  
 QY 121 CTFYALVGIPLEGMLLAGVGDRGSSLRRGIGHIEAFLKWKWVPPGLVRSLSAVFLIG 180  
 Db 159 ciyaliglipqflagvgdqgtifgkiaekvdftikwnvsqtirkiristifilf 218  
 QY 181 CTFYALVGIPLEGMLLAGVGDRGSSLRRGIGHIEAFLKWKWVPPGLVRSLSAVFLIG 240  
 Db 219 cvlfvalpavifkhiedwsaldaiyfvitlttigfgyaggasdiedlfykpvwwfw 278  
 QY 241 LFGLAYFASVLTITGNMRRAVSRRTRAEMGLTAQAASWTGTVA 285  
 Db 279 lvglayfaavvismlgdwlrvisktkeevgefrahaewtanvta 323

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RESULT\_13  
 ID AAE10342  
 ID AAE10342 standard; Protein; 411 AA.  
 XX  
 AC AAE10342;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Murine TREK-1 potassium channel protein.  
 XX  
 Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;  
 KW amnesia.

OS Mus musculus.  
 XX KW insect; TPKC1; human.  
 PN WO200047738-A2.  
 XX OS Homo sapiens.  
 PD 17-AUG-2000.  
 XX XX  
 PF 11-FEB-2000; 2000WO-1B00225.  
 XX PR 12-FEB-1999; 99US-0119727.  
 PR 11-FEB-2000; 2000US-0503089.  
 XX PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PA (BADI ) BASF CORP.  
 PI Lazdunski M, Honore E, Lesage F, Romney G, Patel AJ;  
 XX WPI; 2000-549146-59.  
 DR N-PSDB; AAD17497.  
 XX PT Novel nucleic acid encoding a TREK-1 potassium channel protein for transfecting cells to be used to identify compounds with anesthetic properties -  
 PT XX  
 PS Claim 9: Page 32-33; 39pp; English.  
 XX  
 CC The invention relates to human and mouse TREK-1 potassium channel proteins and their corresponding DNA molecules. TREK-1 nucleic acid is useful for transfecting cells to induce expression of the TREK-1 potassium channel protein. These cells are then used in assays to identify compounds which have anaesthetic properties, producing a safe, reversible state of unconsciousness with concurrent amnesia and analgesia in a mammal upon inhalation. The present sequence is murine TREK-1 potassium channel protein.  
 CC XX Sequence 411 AA,  
 CC SQ  
 PS  
 XX Best, Local Similarity 49.8%; Pred. No. 1.8e-5%; Length 411; Matches 142; Conservative 84; Indels 3; Gaps 1;  
 Qy 1 MRSTTLLALIAVLVLYLVSGLVQALEPHQEQAQKMDHGRDQFLRDHPCVSQSLED 60  
 Db 42 mkwktvstiflwvlyliigavfkaleqpeisqrtrivqkqtflaqpacvnstelde 101  
 Qy 61 FIKLVEALGGGANPETSWTNNSHNSAWNIGSAFFSGTITTCYGTNTVLHTDAGLF 120  
 Db 102 liqgivaaainagip--lgnsnqshwdlgsfftagtvttiqfgnsprrtegkif 158  
 Qy 121 CIFYALVGIPFLFGMLLAGVGDGSSLRGGIGHAEFLKHPPGLVRSLAVELIG 180  
 Db 159 ciyaligipflqfllagvgdqdtifkgikavdftkkwnsqtkiristifilf 218  
 Qy 181 CLLFWLPTFVSYMESWSKLEAIVFVITLTGFDYVPGDGICONSAPAYQPLVFWI 240  
 Db 219 cvlfvalpavikhiedwsaldaiyfwitlttgfdyvaggdsleyldfykpvwwfi 278  
 Qy 241 LFGLAYFASVLTIGNWRASRTRAEMGLTAQASWGTVA 285  
 Db 279 lvglayfaavalsmigrvlrvsktkeevegefrahaewtanva 323  
 RESULT 14  
 AAU07618 ID AAU07618 standard; Protein; 426 AA.  
 XX AC AAU07618:  
 XX DT 21-NOV-2001 (first entry)  
 DE Human potassium ion channel TPKCl protein.  
 XX KW Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelminthic; nematode;

KW insect; TPKC1; human.  
 XX OS Homo sapiens.  
 XX PN WO20161006-A2.  
 XX PD 23-AUG-2001.  
 XX PR 14-FEB-2001; 2001WO-US04680.  
 XX PR 15-FEB-2000; 2000US-0503849.  
 XX PA (BADI ) BASF CORP.  
 XX PI Pausch MH;  
 XX DR N-PSDB; AAS12169.  
 XX PT WPI; 2001-536570/59.  
 PT XX New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions -  
 XX PS Example 15: Page 45; 131pp; English.  
 XX SQ Sequence 426 AA;  
 Qy 1 MRSTTLLALIAVLVLYLVSGLVQALEPHQEQAQKMDHGRDQFLRDHPCVSQSLED 60  
 Best, Local Similarity 49.8%; Pred. No. 1.7e-5%; Length 426; Matches 140; Conservative 57; Mismatches 85; Indels 3; Gaps 1;  
 Qy 57 mkwktvstiflwvlyliigavfkaleqpeisqrtrivqkqtflaqpacvnstelde 116  
 Db 61 FIKLVEALGGGANPETSWTNNSHNSAWNIGSAFFSGTITTCYGTNTVLHTDAGLF 120  
 Qy 174 ciyaligipflqfllagvgdqdtifkgikavdftkkwnsqtkiristifilf 233  
 Db 117 liqgivaaainagip--lgntsnqshwdlgsfftagtvttiqfgnsprrtegkif 173  
 Qy 121 CIFYALVGIPFLFGMLLAGVGDGSSLRGGIGHAEFLKHPPGLVRSLAVELIG 180  
 Db 181 CLLFWLPTFVSYMESWSKLEAIVFVITLTGFDYVPGDGICONSAPAYQPLVFWI 240  
 Qy 234 cvlfvalpavikhiedwsaldaiyfwitlttgfdyvaggdsleyldfykpvwwfi 293  
 Db 241 LFGLAYFASVLTIGNWRASRTRAEMGLTAQASWGTVA 285  
 DB 294 lvglayfaavalsmigrvlrvsktkeevegefrahaewtanva 323  
 RESULT 15  
 AAU07622 ID AAU07622 standard; Protein; 426 AA.  
 XX AC AAU07622:  
 XX DT 21-NOV-2001 (first entry)  
 DE Human potassium ion channel TPKCl mutant protein #1.

XX	KW	Transmembrane potassium ion channel protein; inward potassium flux;
OS	KW	pest control; membrane potential; pesticide; antihelminthic; nematode; insect; TPCK1; human; mutant; muant.
Homo sapiens.		
XX	FH	Location/Qualifiers
	FT	Key-Misc-difference 256 /note= "Wild-type Ala replaced by Thr"
XX	FT	WO200161006-A2.
XX	PN	
XX	PD	23-ABG-2001.
XX	PF	14-FEB-2001; 2001WO-US04680.
XX	PR	15-FEB-2000; 2000US-0503949.
XX	PA	(BADI ) BASF CORP.
XX	PI	Pausch MH;
XX	DR	WPI; 2001-536570/59.
XX	DR	N-PSDB; AAS12181.
PS	PT	New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions
XX	PT	_
XX	PS	Claim 37; Page 113-115; 131pp; English.
XX	CC	The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains comprising mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPCK1 mutant protein.
XX	CC	Sequence 426 AA;
SQ	Query Match 36.3%; Score 755.5; DB 22; Length 426; Best Local Similarity 48.8%; Pred. No. 3.7e-56; Matches 139; Conservative 57; Mismatches 86; Index 3; Gaps 0	
QY	1 MRSTLIALLALVLLVLSGALVFQALEQQHEQQAQKMDHRDQLRDLFPCVSOKSLED 60	
Db	57 mkwktvstiflqvwyliqatvkaleqheisqrtrivqkqfisqscvnstelde 116	
QY	61 FIKLVLVEGGANPETSWNNSNNSAWNNGSAFFSGTTTGYGNVLTHTDAGRIF 120	
Db	117 liqqiyavaanagiip--lqtnsqnqishwalgnsfrfragitttqgnnsprteggkif 173	
QY	121 CIFYALVGPILEFGMLLAGVGDRLGSSLRGIGHIEAFLKWHVPGPLVRSLSAVLFIG 180	
Db	174 ciiyaligipiifgflaqvdqglqftgkqikavdftfkwnvsqtirkistitiflg 233	
QY	181 CLLFVLPTEFVFSYMEWSKIEAKIIVVIVLITVGFDDYPPGDGTQNSAYQPLWFWI 240	
Db	234 ovlfvalpalifkhiegwslasdtykvitlttgfdyraggsdleyldfykpvwfw 293	
QY	241 LFLGLAVFASVITPTGTMWLRVLAISRRTRAEMLTAQDASWNTVTA 285	
Db	294 lvglavafaavismiglvrviskkteeveefrahaewianvta 338	

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GenCore version 4.5

**OM protein - protein search, using sw model**

Run on:	June 4, 2002, 10:58:30 ; Search time 14.74 Seconds	(without alignments)
Scoring table:	BLOSUM62	659.524 Million cell updates/sec
Searched:	231628 seqs, 24425594 residues	
Total number of hits satisfying chosen parameters:	231628	

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

**Database :**

- 1: Issued\_Patents\_AA:\*
- 1: /cgn2\_6/ptodata/2/1aa/5B\_\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/5B\_\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/pctUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/packfiles1.pep:\*

.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Length	DB ID	Description
1	776.5	37.3	411	US-09-236-080-2 Sequence 2, Appli
2	770.5	37.1	411	US-09-236-080-6 Sequence 6, Appli
3	761.5	36.6	370	US-09-144-914-8 Sequence 8, Appli
4	379.5	18.3	336	US-08-749-810-2 Sequence 2, Appli
5	379.5	18.3	336	US-09-144-914-2 Sequence 6, Appli
6	343	16.5	107	US-09-236-080-4 Sequence 4, Appli
7	332.5	16.5	405	US-09-144-914-5 Sequence 5, Appli
8	326.5	15.7	394	US-09-144-914-4 Sequence 4, Appli
9	301.5	14.5	616	US-08-332-312-2 Sequence 2, Appli
10	209	10.1	336	US-08-332-312-4 Sequence 4, Appli
11	198	9.5	383	US-08-749-816-4 Sequence 7, Appli
12	198	9.5	383	US-09-144-914-7 Sequence 3, Appli
13	184.5	8.9	347	US-08-749-816-3 Sequence 6, Appli
14	184.5	8.9	347	US-09-144-914-6 Sequence 4, Appli
15	132	6.3	696	US-08-906-865-6 Sequence 4, Appli
16	122	5.9	1593	US-08-628-829-4 Sequence 13, Appli
17	118	5.7	1159	US-08-956-242-13 Sequence 1, Appli
18	118	5.7	1159	US-09-351-215-13 Sequence 13, Appli
19	118	5.7	1159	US-09-226-012-2 Sequence 2, Appli
20	118	5.7	1159	US-09-226-012-4 Sequence 4, Appli
21	117	5.6	1083	US-09-600-776-2 Sequence 2, Appli
22	113	5.4	2293	US-09-368-590-2 Sequence 2, Appli
23	111.5	5.4	2293	US-09-135-020-114 Sequence 114, App
24	111.5	5.4	570	US-09-135-010A-114 Sequence 114, App
25	111.5	5.4	581	US-09-135-021-80 Sequence 80, App
26	111.5	5.4	4	US-09-135-010A-116 Sequence 116, App
27	111.5	5.4	676	US-09-135-021-2 Sequence 2, Appli





QY 7 LALLALVLLYLIVSGALVFOALEOPHEQQAKKMDHGRDPLRHPVCYSOKSLDFIKLV 66  
Db 6 LALIVCTETYLTVLGVAVFALESPMEERQRQREL-ROLELRARYNLSSEGYYEELERVVL 64  
QY 67 BALGGGANPETSWNNSNHSANLGSAFFESTTITIGVGNIVLHTDAGRLFCFVAL 126  
Db 65 RLKPHKAGVQ-.....WRFAGSFYATVITVITGQHAAFSPTDGKVFCMFYAL 112  
QY 127 VGIPLFGMLLAGVQDRGSSLR-----RGIG---HTEAIFLKWHVPGLVLSAVLFL 177  
Db 113 LGIPLTLIMEQSIGERINIFVRILHRAKGIGMRHAE-----SMMANVLIG 160  
QY 178 LGICLFLFVLTPTFVFSYMSWMSKLEAIYFVITLTIVFGDYV--PDGTGONSPAYQPL 235  
Db 161 FVSCISTICIGAAAFSYERWTFFOAYYCFITLTIGFGDVVALQKDQALQTQPOY-- 217  
QY 236 WMIWILEGLAYFAASVLTIGNWIRAVSR 264  
Db 218 ---VAFSFVYILTGTVIGAPLNLVLR 242

RESULT 8  
US 09-144-914-4  
; Sequence 4, Application US/09144914  
; Patent No. 6309855  
; GENERAL INFORMATION:  
; APPLICANT: Duprat, Fabrice  
; APPLICANT: Lesage, Florian  
; APPLICANT: Fink, Michel  
; APPLICANT: Lazdunski, Michel  
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS  
; FILE REFERENCE: 989.6705CIP  
; CURRENT APPLICATION NUMBER: US/09/144, 914  
; CURRENT FILING DATE: 1998-03-01  
; EARLIER APPLICATION NUMBER: 08/749, 816  
; EARLIER FILING DATE: 1996-11-15  
; EARLIER APPLICATION NUMBER: 60/095, 234  
; EARLIER FILING DATE: 1998-08-04  
; EARLIER APPLICATION NUMBER: FR 96/01565  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 4  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: OTHER INFORMATION: TASK  
; ; US-09-144-914-4

Query Match 15.7%; Score 326.5; DB 4; Length 394;  
Best Local Similarity 31.5%; Pred. No. 1.2e-19; Matches 85; Conservative 45; Mismatches 95; Indels 45; Gaps 7;

QY 7 LALLALVLLYLIVSGALVFOALEOPHEQQAKKMDHGRDPLRHPVCYSOKSLDFIKLV 66  
Db 9 LALIVCTETYLTVLGVAVFALESPMEERQRQREL-ROLELRARYNLSSEGYYEELERVVL 67  
QY 67 BALGGGANPETSWNNSNHSANLGSAFFESTTITIGVGNIVLHTDAGRLFCFVAL 126  
Db 68 RLKPHKAGVQ-.....WRFAGSFYATVITVITGQHAAFSPTDGKVFCMFYAL 112  
QY 127 VGIPLFGMLLAGVQDRGSSLR-----RGIG---HTEAIFLKWHVPGLVLSAVLFL 177  
Db 116 LGIPLTLIMEQSIGERINIFVRILHRAKGIGMRHAE-----SMMANVLIG 160  
QY 180 G---CLFLVLTPTFVFSYMSWMSKLEAIYFVITLTIVFGDYV--PDGTGONSPAYQPL 234  
Db 163 GFSSCISTICIGAAAFSYERWTFFOAYYCFITLTIGFGDVVALQKDQALQTQPOY-- 220

QY 235 LVWFWLGLAYFAASVLTIGNWIRAVSR 264  
Db 221 ---VAFSFVYILTGTVIGAPLNLVLR 242

RESULT 9  
US-08-332-312-2  
; Sequence 2, Application US/08332312  
; Patent No. 559026  
; GENERAL INFORMATION:  
; APPLICANT: Price, Laura A.  
; APPLICANT: Pausch, Mark H.  
; TITLE OF INVENTION: Functional Expression of a Drosophila  
; TITLE OF INVENTION: Melanagaster Putative Potassium Channel in Yeast  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: US  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/332,312  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: P-36,711  
; REFERENCE/DOCKET NUMBER: 32,421  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3246  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 618 amino acids  
; TOPLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-332-312-2

Query Match 14.5%; Score 301.5; DB 1; Length 618;  
Best Local Similarity 27.7%; Pred. No. 2.6e-17; Matches 91; Mismatches 111; Indels 75; Gaps 10;

QY 7 LALLALVLLYLIVSGALVFOALEOPHEQQAKKMDHGRDPLRHPVCYSOKSLDFIKLV 66  
Db 7 ILLIIFYISLYMFGAIIYHIE-----HGEEKKSAROKKAIAINTY---LL 51  
QY 67 BALGGG-----ANPETSWNNSNHSANLGSAFFESTTITIGVGNIVLHTDAGRLFCFVAL 110  
Db 52 EELGDKNTTDEQLQRISYCDKPVTLPPRTDPPYTFWYAFFATWCSTIVIGNI 111  
QY 111 VLHTDAGRRLFCFVALVGILFGMLLAGVQDRGSSLRREGIGHTEAIFLKWH----- 161  
Db 112 SPTTFAGRMIMIAYSVIGTYFVNGTFLAGGEYFGRT-----FEAIRRYKKYKSTMID 164  
QY 162 -HVPPGLVRSLSAVFLPLGCLFLVLPTRP-VFSYMSWMSKLEAIYFVITLTIVFGDY 219  
Db 165 HYVPFQGLITITVIALPQIALEVLVLPVGVLHREGLISSLYSYVTTTIGRDY 224  
QY 220 VPGDGTTGQNSP-----AYCOPLWFLGLAYFAASVLTIGNWIRAVSRRAEMGIL 273  
Db 225 VPTFGANOPKEFGWFWVQIQIVWFLFSLGYLVMIMPITRGLQS----KKLAYE 278  
QY 274 AQAS-----WTGTVARYQRTG 292



TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

FILE REFERENCE: 989\_6705CIP

CURRENT APPLICATION NUMBER: US/09/144, 914

EARLIER FILING DATE: 198-09-01

EARLIER APPLICATION NUMBER: 08/749, 816

EARLIER APPLICATION NUMBER: 60/095, 234

EARLIER FILING DATE: 198-08-04

EARLIER APPLICATION NUMBER: FR 96/01565

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 7

LENGTH: 383

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog  
US-09-144-914-7Query Match 9.5%; Score 198; DB 4; Length 383;  
Best Local Similarity 26.7%; Pred. No. 6.5e-07;  
Matches 60; Conservative 42; Mismatches 95; Indels 28; Gaps 6;Qy 9 LLALVLVLYLVSALVQALEQH-E-QQAOKKMDHGRDQFLRDHPC--VSQSKLEDF 61  
Db 44 LVLSCTVYALGAYLFSLIEHPEELRKREKATREFQDLQDFMGNTSGIENSEIY 103  
Qy 62 IKLVEALGGGANP--ETSWTNSNHSAAWNLGSARFFSGCTITITIGYGNVILHDAGR 118  
Db 104 TKKLILMELDAHNAHAEYEFFINHEPKDMWTFSSALVFTTIVPGYGYIFPVSAIGR 163  
Qy 119 LFCIFYALVGILFGMLLAGYDGRGSSLRQIGHTEAFLKWHVPPGLVRSLSAVLF 178  
Db 164 MCLIAVALGIGLTLVIMADQKFAAQOLVTRFEGDN-----MAIPAIFI- 209  
Qy 179 ICLLFVY--LTPTFVFSYMESESPLSKLAIYFVITLTWGRGDYVP 221  
Db 210 --CLLFYPLVVGFFLCTSNTYLDHSVFSLTSIFTIGRQLTP 252

RESULT 13

US-08-749-816-3

Sequence 3, Application US/08749816

Patent No. 6013470

GENERAL INFORMATION:

APPLICANT: Lesage, Florian

APPLICANT: Guillemare, Eric

APPLICANT: Duprat, Fabrice

APPLICANT: Lazdunski, Michel

APPLICANT: Romey, Georges

APPLICANT: Barbinin, Jacques

APPLICANT: FAMILY OF MAMMALIAN POTASSIUM CHANNELS

TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING

TITLE OF INVENTION: OF DRUGS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER &amp; ASSOCIATES

STREET: 230 South Fifteenth Street, Suite 500

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/749, 816

FILING DATE: 15-NOV-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerrard J.

REGISTRATION NUMBER: 19, 763

REFERENCE/DOCKET NUMBER: 999.6351P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 347 amino acids

TOPOLOGY: linear

STRANDEDNESS:

MOLECULE TYPE: protein

US-08-749-816-3

Query Match 8.9%; Score 184.5; DB 3; Length 347;  
Best Local Similarity 25.8%; Pred. No. 7.7e-08;  
Matches 69; Conservative 41; Mismatches 74; Indels 83; Gaps 11;Qy 6 LLALVLVLYLVSALVQALEQH-E-QQAOKKMDHGRDQFLRDHPC-SQSLEDFKLL 65  
Db 40 LSAAITLVLNFN-LGAGIVTYLAQNSES-----LNENSES-KCLHL--- 82  
Qy 66 VEALGGGANPETS-----WTNSNHSSAWNLGSAFFSGTTITIGYGNVILHDAGR 119  
Db 83 --PIGGKITAEMKSKLKGKLTKSRRD--GEKAIFPSWLYTIVGYSLYPHSTGRY 137  
Qy 120 FCIFYALVSGTPL-----FGMLLAG--VGURIGSIRR-----G 151  
Db 138 LTIVSVLIMPVTFAKFEEGTFLAHFLVWVSNRTRLAKKAYKYLSONPENAFTPSNL 197  
Qy 152 GHTEAFLKWHVPPGLVRSLSAVLFLLGCLLVEVLPFPFVFESMESPLSKLAIYFVTL 211  
Db 198 QHDYLFLS-----SLICLSSLSSAFLSSIENISYLSVYFGITM 241  
Qy 212 TTVSRGDYVPGDGTQONSAPQYPLWF 238  
Db 242 FLIGDIVPTN-----LVWF 257

RESULT 14

US-08-144-914-6

Sequence 6, Application US/09144914

Patent No. 630955

GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice

APPLICANT: Lesge, Florian

APPLICANT: Lazdunski, Michel

APPLICANT: Romey, Georges

APPLICANT: FAMILY OF MAMMALIAN POTASSIUM CHANNELS

TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING

TITLE OF INVENTION: OF DRUGS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER &amp; ASSOCIATES

STREET: 230 South Fifteenth Street, Suite 500

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/749, 816

FILING DATE: 15-NOV-1996

OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog  
US-09-144-914-6

Query Match 8.9%; Score 184.5; DB 4; Length 347;  
 Best Local Similarity 25.8%; Pred No. 7.7e-08; Indels 83; Gaps 11;  
 Matches 69; Conservative 41; Mismatches 74; Del 11;

Qy 6 LLALALALVLYLIVSGALIVFOALQSPHEOAQKMDHGQDFLRDHPSQSKLEDFIKLL 65  
 Db 40 LSAATITLVLVNL-GAGIFYLAPEONSES-----INNSEVS-KCBLNL--- 82

Qy 66 VEALGGGANPETS----WTTNSNHSSAWNLGSAFFSGTTTIGGNVLTADGRL 119  
 Db 83 --PGGGKTAEMMSKLKGKLTSSRID--GECKAIFPSWTIYSTVYGSILPHSTGRY 137

Qy 120 FCTTYALVSIPL-----FGMLLAG---VGDRGLSSLR-----GI 151  
 Db 138 LTIFYSLMIPVIAFKFEGFTLAHFLVVNSRTRLAVKAYKYLSONPENAPTPNSL 197

Qy 152 GHIAIFLKWHPGLVLSASVLFLLGCLLVLTPFVFSMESKLEYFYVLT 211  
 Db 198 QHDYLILFLS-----SLLCSISLSSALFSSSIENISYLSWYFGITM 241

Qy 212 TTVGFGDXYWPGDGNGQNSPAYQDQW 238  
 Db 242 FLIGIGDQVPTN-----LVWF 257

Search completed: June 4, 2002, 11:00:34  
 Job time: 124 sec

Query Match 6.3%; Score 132; DB 3; Length 696;  
 Best Local Similarity 28.8%; Pred. No. 0.0048; Indels 46; Gaps 5;  
 Matches 42; Conservative 16; Mismatches 42; Del 11;

Qy 289 QRTGP---SAPPKEEQL-----IPLSSLAPPAYVEP----- 318  
 Db 475 QRQGPPLQQRPQGQHLSLGPPRGSPSPQRQTSQPSQARPTQOGGRSR 534

Qy 319 -AGRCPSPAPREKEVTPSPRTASALDYPNSNLAFTIDESDTSRGCALPRA---PIG 372  
 Db 535 PYAGGPGAPPAARPPASP-----ORQAGPPOQRTQTSVSGPAPKASGAPPG 584

Qy 373 RIRPNISKPSRPGGRLRKAVPV 398  
 Db 585 QORQGPQPKPPGAPGPTRQASQAGPV 610

RESULT 15  
 US-08-906-865-4  
 ; Sequence 4, Application US/08906865  
 ; Patent No. 6040168

GENERAL INFORMATION:

APPLICANT: Greenard, Paul  
 APPLICANT: Kao, Hung-Teh  
 APPLICANT: Porton, Barbara

TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.  
 STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 STREET: Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,865  
 FILING DATE:  
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-202

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 696 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: /desc = "Synapsin Ia"  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

US-08-906-865-4

Tue Jun 4 11:44:25 2002

us-09-655-272-2.rai

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 4, 2002, 10:58:45 ; Search time 20.89 Seconds  
 (without alignments)  
 1830.711 Million cell updates/sec

Title: US-09-655-272-2  
 Perfect score: 2079  
 Sequence: I MRSTLALLALVALVLYLVSG . . . . . SKKFSRPRGPGRLLDKAVPV 398

Scoring table: BLOSUM62

Gapop 10.0 , Gabext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : PIR 71.1:  
 1: pir1;\*  
 2: pir2;\*  
 3: pir3;\*  
 4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	379.5	18 3	336 2	inward rectifier potassium channel TWIK-1 - human
2	353	17 0	1001 2	potassium channel TASK-5 protein - h
3	323.5	15 6	330 2	probable potassium outward rectifier
4	322	15 5	329 2	probable potassium probable potassium
5	314.5	15 1	336 2	hypothetical protein
6	298.5	14 4	364 2	hypothetical protein
7	291.5	14 0	334 2	hypothetical protein
8	279	13 4	528 2	hypothetical protein
9	269.5	13 0	392 2	hypothetical protein
10	269	12 9	524 2	hypothetical protein
11	265	12 7	393 2	hypothetical protein
12	261.5	12 6	443 2	hypothetical protein
13	257.5	12 4	522 2	hypothetical protein
14	248.5	12 0	513 2	hypothetical protein
15	242.5	11 7	1910 2	protein TWIC9_3 [i]
16	242	11 6	643 2	hypothetical protein
17	240.5	11 5	325 2	hypothetical protein
18	240	11 5	461 2	potassium channel
19	236.5	11 4	452 2	hypothetical protein
20	236.5	11 2	307 2	hypothetical protein
21	232.5	11 1	539 2	hypothetical protein
22	231.5	11 1	1539 2	hypothetical protein
23	230	11 0	551 2	hypothetical protein
24	229	11 0	555 2	hypothetical protein
25	229	11 0	557 2	hypothetical protein
26	228	11 0	485 2	hypothetical protein
27	223	10 7	444 2	hypothetical protein
28	222	10 5	305 2	hypothetical protein
29	218.5	10 5	484 2	probable potassium

#### ALIGNMENTS

RESULT 1

Query Match 18.3%; Score 379.5; DB 2; Length 336;  
 Best Local Similarity 34.4%; Pred. No. 2.2e-17; Mismatches 95; Indels 23; Gaps 9;

Matches 90; Conservative 54; MisMatches 9;

Query RSTLALLAL-VLYLVSGALVQALEQPHEQQAQKMDHQDQFLRDPCVSQSKLED 60  
 Db 18 RSAWCFGELVLGVLYLVGAWFVSSWELLPLDRLLKLRRFLEREECLSEQLEO 77  
 Qy 61 FIKLIVEALAGGG---ANETSWINNSNHSSAWNLGSAFFSGTIIITIGGNIVLHTDA 116  
 Db 78 FLGRVLEASNYGVSLNSAASNQWN----WDFTSALFFASTVLISTTGXGHTVPLSDG 129  
 Qy 117 GRLCIFCIALVWGLPLFGMLLAGVGDRGLSSL-RRGIGHTEAIFLKWHVPPGLVRSLAVL 175  
 Db 130 GKAFCITYSVIGIPTFLFLFTAVQRITVHVIRRPLVYFH--IRMGFSKQVVAHVYL 186  
 Qy 176 -FLIGLICLFLVTPFESYME-SWSKSLAEIYFVIVLTVGFGDXVPGDGDTGON-SPA 231  
 Db 187 LGFVIVSCHFFI-PAAVSVLFDWWNPLESFYFCFISLTIGLGDVPGEGYNQKFEL 244  
 Qy 232 YQPLVWFWILFLGAYFASVLF 253  
 Db 245 YKIGITCYLLGLIAMLVLET 266

#### RESULT 2

Query Match 18.3%; Score 379.5; DB 2; Length 336;  
 Best Local Similarity 34.4%; Pred. No. 2.2e-17; Mismatches 95; Indels 23; Gaps 9;

Matches 90; Conservative 54; MisMatches 9;

Query T16629 10.5%; Score 335.2; Db 544635 10.4%;  
 C;Species: Drosophila melanogaster  
 C;Date: 13-Aug-1997 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
 C;Accession: T13807  
 R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.  
 Proc. Natl. Acad. Sci. U.S.A., 93, 1325-1326, 1996  
 A;Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster  
 A;Reference number: Z17770; MUID:97075152

A;Accession: T13807  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-1001 <GOL>  
A;Cross-references: EMBL:U55321; NID:93808067; PID:93808068; PTDN: AAC69250.1  
C;Genetics:  
A;Gene: ORK1  
A;Cross-references: FlyBase:FBgn0017561  
A;Map position: 1

Query Match 17.0%; Score 353; DB 2; Length 1001;  
Best local Similarity 29.1%; Pred. No. 3.4e-15; Mismatches 95; Conservatve 54; Indels 74; Gaps 9; Matches 95;

QY 7 LALIALVILVLYSVALVSGALVQEALPQPHQEQAKKMDHGRDQFLRDPVCVSQSKSLDEDIKLV 66  
Db 7 ILLIIFYISYLMEGAATYHIE-----HGEKTSAEORKAQTAINEY---LL 51

QY 67 EAJGGG-----ANPESWNTNSNHSSAWNLCSAFFSGSGITITIGYNI 110  
Db 52 EELGDKNNTTQDEBILQRISDYCDKPVNLTPTVTPWTYHAEFAFTCSTVGYN 111

QY 111 VLIHDAGRLFCFVYALVGLPIGLLAVGDRIGSSLRRGIGHIEAFLKN----- 161  
Db 112 SPTFFAGRVMIMATVSGVPGVNGIPGLRAGLGIVFGRT-----FEAIYRKYKYMSTM 164

QY 162 -HVPVGLVRSLSAVLFULLGICLFLVTPTEFVSYMSWKSLEAIYVIVLTVGFGDV 220  
Db 165 HVPVQLQLITIVVIALIPGLFLPLPSWTFYENWPVPSISLYSYVMTTGFDV 224

QY 221 PEGDTGONSP-----AYOPLFWLFLGLAYFASVLTIGNLRAVSRTRRAEMGLTA 274  
Db 225 PTFGANOPKERFGFWVYQIRVIVWFLFISLGVLVMMTFTGRGLOS-----KKLAYEQ 278

QY 275 QAS-----WGTGIVTARVHQRC 292  
Db 279 QISSNLKATQNRIWSG-----VTKDVG 300

RESULT 3  
JCT703

C;Species: Homo sapiens (man)  
C;Accession: JCT703  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C;Accession: JCT703  
C;Title: TASK-5, a new member of the tandem pore K<sup>+</sup> channel family.  
A;Reference number: JCT703; MOID:21303050; PMID:1140881  
A;Accession: JCT703  
A;Molecule type: DNA  
A;Residues: 1-330 <KIM>  
A;Cross-references: GB:AU118522  
C;Comment: This protein, a new member of the tandem-pore K<sup>+</sup> channel family with four transmembrane segments, but does not produce a functional plasma membrane K<sup>+</sup> current by itself.  
C;Genetics:  
A;Gene: task-5  
A;Map position: 20q12  
C;Keywords: transmembrane protein  
F;7-30/Domain: transmembrane segment #status predicted <TMS1>  
F;107-128/Domain: transmembrane segment #status predicted <TMS2>  
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted  
F;156-180/Domain: transmembrane segment #status predicted <TMS3>  
F;220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 15.6%; Score 323.5; DB 2; Length 330;  
Best Local Similarity 28.7%; Pred. No. 8.5e-14; Mismatches 110; Conservatve 48; Indels 75; Gaps 14;

QY 3 STIULLALLAIVLYLVSGLVFALEQPHQEQAKKMDHGRDQFLRDPVCVSQSKSLDEDIKV 62

RESULT 5  
T32347

Db 5 SVRAAGLVLICLTCYLVLGAAGDALESEAESGRQRLLVKRGALRKFCF---SAEDYR 60  
QY 63 KLLVEALGGGANPETSWTNSNHSSAWNLCSAFFSGSGITITIGYNTLHTDAGRLLC 122  
Db 61 EL--ERLAQAEPHA----GRQWKPGSFFAITVTTIGYHAPGTSGKVCC 111

QY 123 FYALVGIPFLGMLLAGVGDRIGSSLRRGIGHIE-AIFLWVHPGVLVRSLSAVLFLIC 181  
Db 112 FYALIGIPLTLVTFOSIGERLNAAVRLLAACKCCLIGLW---TCVSTENLVAGLAC 167

QY 182 LLFVLTPTFVSYMSWSKLEAIYVIVLTVGFGDV---PGDGTCQNSPAYQPLVWF 238  
Db 168 AATLALGAVAVRSRFFGWTFPHAYYCFTTITGFGDFVALQSGEALQRKLP----- 219

QY 239 WILFGIAYFASVLTIGNLRAVSRTRRAEMGLTAQASWIGTVTARTVQTGSPAPP- 297  
Db 220 YVAFSFLYFLGLTVGATLNLVLR-----FLVASADWPERAA-----RKPSPRPG 267

QY 298 -PEKEQPLPSSLAPPAYVAPCRGPSPSA---PAEKVETPSPTASALDYPSENLAFIGD 353  
Db 268 APESRGLWLRP-----RPARSVGSASFVCHVHLERCA-----RDNLGFSP 308

QY 354 ESDTQSERGCALPAPRPRRRP 376  
Db 309 PSS-----PGVVRGQAP 321

RESULT 4  
T43509

C;Species: Caenorhabditis elegans  
C;Accession: T43509  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
C;Accession: T43509  
R;Wang, Z. W.; Salkoff, L.  
submitted to the EMBL Data Library, August 1998  
A;Description: Potassium channels in C. elegans.  
A;Reference number: Z22450  
A;Accession: T43509  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-329 <WAN>  
A;Cross-references: EMBL:AF083652; PIDN: AAC32863.1

Query Match 15.5%; Score 322; DB 2; Length 329;  
Best local Similarity 31.5%; Pred. No. 1.1e-13; Mismatches 93; Conservatve 45; Indels 44; Gaps 9; Matches 93;

QY 7 LALIALVILVLYSVALVSGALVQEALPQPHQEQAKKMDHGRDQFLRDPVCVSQSKSLDEDIKLV 66  
Db 9 LSLIVCLTLYLVLGAAYVDALETTENELTQLKLVYREKTKY---NNNSNADY---- 59

QY 67 EAJGGGANPETSWTNSNHSSA-WNLCSAFFSGSGITITIGYNIVLHDAGRFCITY 124  
Db 60 EIL-----EATIVKSPHKAGYQWIKESGAYFATVITIGYHGPMDAGVFCMY 113

QY 125 ALVGIPFLGMLLAGVGDRIGSSLRRGIGHIEAFLWVHPGVLVRSLSAVLFL 177  
Db 114 ALAGIPLGLIMPQSIGERMNFAKURFIRRAAG-----KQPVTSSDLIIFC 162

QY 178 LGCLLIPVTPFVFSMESWSKLEAIYVIVLTVGFGDV- PGDGTCQNSPAYQPL 235  
Db 163 TWGGGLLIFGGAFMFSSYYNNTYFDAYYCFVLTIGFDYVALQKRGSLQTOPEVYFF 222

QY 236 VWFVLTPTFVSYMSWSKLEAIYVIVLTVGFGDV---LTAQASWIGTVIA 285  
Db 223 SLVFILFLGTVISAAMNL--VLRFLETMNEDERDEOEAILAAQGLVRYGVDPFA 275

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999

C;Accession: T32347

A;Molecule type: DNA

A;Residues: 1-336 <MUR>

A;Cross-references: EMBL:AF025454; PIDN:AC71151.1; GSPDB:GN00020; CESP:F34D6.3

A;Experimental source: strain Bristol N2; clone F34D6

A;Genetics:

A;Map position: 2

A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match

Best Local Similarity 15.1%; Score 314.5; DB 2; Length 336; Matches 94; Conservative 43; Mismatches 118; Indels 43; Gaps 9;

QY 7 LALIALVALVLVLYSVALVQALEQPHEDQAKKMDHGRDQLRHPVSQK---SLDFIK 63

Db 9 LSLIVCTYLILVYGAVIDELENTEIQLVQRGIEPRLVQVRKTKYNNSNADY- 66

QY 64 LLVALGGGANPETSWTNNSNHSSA- WNLGSAFFSCITITIGKGNVLHTDAGRIFC 121

Db . 67 ---ELI-----EATIVKSPHRYAQWKFSAFYFAITVITIGKHSPTKMDACKYFC 117

QY 122 IFYALVGIPFLFGMLLAGVGDRUGS-----SLRRGIGHIEAFLKWHVPPGLVRSLSAV 174

Db '118 MYALAGIFPLGLIMFOSIGERMTFAAKLRFIRRAG-----KQPIVTSSDLI 166

QY 175 LFLIJLGCLFLVLPFTVSYMSWKSKEIAIFVIVVLTWVGDDYV--PGDGTGONSPAY 232

Db . 167 IFCYTGWGGGLIFGGAFMSSSYWNTYFAAVYCFVTLITIGFDYVALQQKRSLSQTQPEY 226

QY 233 QPLVFWFILFLGLAYFASVLTITGNWLRAVSRRTRAEMG---LTAQASASWGTVA 285

Db 227 VFEFLVLFILFLGLTVISAAMNL--VLRFLTMNTEDEERDEQEARAILAOGLVRVGDPTA 282

RESULT 6

T43361 probable potassium channel chain n2P20 - Caenorhabditis elegans

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

C;Accession: T43361

R;Wang, Z.W.; Salkoff, L.

A;Submitted to the EMBL Data Library, August 1998

A;Description: Potassium channels in *C. elegans*.

A;Reference number: Z22450

A;Accession: T43361

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-364 <WAN>

A;Cross-references: EMBL:AF083646; PIDN:ACC32857.1

Query Match

Best Local Similarity 14.0%; Score 291.5; DB 2; Length 334; Matches 82; Conservative 59; Mismatches 116; Indels 45; Gaps 8;

QY 2 RSTTLALLALVALVLVLYSVALVQALEQPHEDQAKKMDHGRDQLRHPVSOKSLED 61

Db 7 KSARALLLILSTFTYLFAGMVFDKLESERDTWREDEIERITD-LKHKNFSERDHLF 65

QY 62 IKLVALGGGANPETSWTNNSNHSSAWNLGSAFFSCITITIGKGNVLHTDAGRIFC 121

Db 66 EAIAIKSIPQOQGYQ-----WOFAGAFYFAITVITVGHHSAPSTWAGKLFC 113

QY 122 IFYALVGIPFLFGMLLAGVGDRUGS-----RGHIGHIEAFLKWHVPPGLVRSLSAV 175

Db . 114 MIFALFGVPMPGLIMFOSIGERVNTEFAYSHLKFRDSLHOOQFTCLOEVTPHLLMS-- 170

QY 176 FLLIGCLFLVLPFTVSYMSWKSKEIAIFVIVVLTWVGDDYVPPGDTG - ONSPAVQ 233

Db 171 -LTIG-FMIVIVSGTYMEHTIKWSKSDAYFCMITSPTIGFGLDVFLQQNALQDPLIV 228

Db 234 PLVFWFILFLGLAYFASVLTITGNWLRAVSRRTRAEMG-LTAQASASWGTVAUTGP 293

Db 229 FATIMFLILGLAVFSAVNLL-----VLGFMASNADEVA - AQREPP 269

QY 294 SA 295

Db 270 SA 271

RESULT 8

T21834 hypothetical protein F36A2.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T21834  
 R;Lennard, N.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: Z19476  
 A;Accession: T21834  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-528 <WIL>  
 A;Cross-references: EMBL:Z81077; PIDN:CAB03071.1; GSPDB:GN00019; CESP:F36A2.4  
 C;Genetics:  
 A;Gene: CESP:F36A2.4  
 A;Map position: 1  
 A;Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1  
 Query Match 13.4%; Score 279; DB 2; Length 528;  
 Best Local Similarity 23.0%; Pred. No. 1e-10;  
 Matches 107; Conservative 53; Mismatches 126; Indels 180; Gaps 16;  
 Qy 9 LIALAVLILYLVSGALVFGALEQPH-----  
 Db 21 LIGGSWVILVILGAIIVFOMIEGLHDNFSDFNPKHHFGPKMVDFKFFETIFRRWSKGANFKK 80  
 Qy 32 -----ECQADRKMD----HGRDQFLRDPHCVSOKSLEDFIKLVEALGGGA 73  
 Db 81 SALKKDHMAKL-EQNAKYVDKLVSWAKRDRKY-----KVNEDLIKSVKEDTVDD 131  
 Qy 74 NPETSWP-----NSSNNSSAWNNGSAFFSGFTITTTGGNTVLTDAQRUCIFY 124  
 Db 132 NDYVDTFYAHRAVRHGYYDEPSWTWFANSFTTMLTSIGGYWAPSTFGRLFGVIY 191  
 Qy 125 ALVGIPFLGMLLAGVGDRLGSL-----RRGIGHIEAIFLK----- 160  
 Db 192 CLIGIPLTLVTVANVAFKLSEPTFFLYELANNKCLEMRKRKGGEVEDPLOPMFGDENE 251  
 Qy 161 -----WHVPPGLVLRSLSAWLFLL-GCLFLFVLTPTFVFSYMSWSKLEAVIYFVVT 210  
 Db 252 EELLDVRVLRVFP-----LAFFFFVFWYGC-----AAWVWVRYWEIWTVYESLYFIS 301  
 Qy 211 LTTVGVGRDYVPGDGTSQSPAYQVLPWFVWILFGLAYFASVLT-----I 254  
 Db 302 ILTVGFDGDIRPSPGN-----IWVTLIAFWVVGVLITMCMDVGRMYLKEHYL 349  
 Qy 255 GNWLRL-----AVSRRTAEMGLTAQAAASWGTWTA-----RVTQR 290  
 Db 350 GRKLKSSSNPFYLIREAKARRRKAAMASLLAQAK-GMIFAHKDYNELARKSKRKREKR 407  
 Qy 291 TGPSSAPPEKEQ-PLPSSLAPAPAVPEA-----GRCPGPAP 327  
 Db 408 RGSHVLPNEKFMPARLPPDPSCDQVSTAYSVRLAWAPPESPD 453  
 .  
 RESULT 9  
 T23907  
 Hypothetical protein R04F11.4 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T23907  
 R;Harris, B.  
 submitted to the EMBL Data Library, June 1996  
 A;Reference number: Z19816  
 A;Accession: T23907  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-524 <WIL>  
 A;Cross-references: EMBL:Z74475; PIDN:CAA98957.1; GSPDB:GN00023; CESP:R04F11.4  
 A;Experimental source: clone R04F11  
 C;Genetics:  
 A;Gene: CESP:R04F11.4  
 A;Map position: 5  
 A;Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2  
 .  
 Query Match 12.9%; Score 269; DB 2; Length 524;  
 Best Local Similarity 23.0%; Pred. No. 4.e-10;  
 Matches 123; Conservative 58; Mismatches 139; Indels 214; Gaps 21;  
 Qy 7 LAL---LALVL---YVSGALVFGALEQPHQHQQAOKR-----MDH-----  
 Db 11 LALPHGFLVLISIGTYLIGALCFHHYERPYEQLNRNETSRRIGELKNRVMQLWRMSNN 70  
 Qy 42 -----GRDQFLRDPHCVSOKSLEDFIKLVEALGGGANPETSNTNSNH-----  
 Db 71 TAYSTWROTANDGMDELIR-----VFDYTRNMTP 103  
 Qy 88 -----AWNLGSAFFSGFTITTTGGNTVLTDAQRUCIFY 138  
 Db 104 DVYGDGPIKNSFMSSIFFSWTAITTIGGHVPRIDEGRVIAITYALLGIPLWVIA 163  
 Qy 139 VGDRLGSS--SLRGGIGHIEAIF-----IKW-----HYP-----  
 Db 164 IGRFLATVYIKLHGYMAVMSFVNTSCLCJCKWACWIRLPRHLPMPTELLORTOKY 223

QY 165 ----- PGLYRSLS----- 172  
 Db 224 PNNNNPTVAAATAASAGGGTGRKKOORDNVSDAGTFDNLSEINDSEGGENENEGEEEQ 283  
 QY 173 -----AVLFILIGCLFLVLTPTFVFSYMEWSKLEAIFYVFLVLTWFGFGDV 220  
 ; |||: | :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 284 IQDPSPNHEKRVSYVFLIMGYYVAGAYIVWRWBETWFEAFYFCFVWTTGFGDLY 343  
 QY 221 PGDGTGQNSPAYPLWFWFLLFGLAYFASVLTIGN-WLRVSRKTRA----- EMGLIT 273  
 | :|||: |||: |||: |||: |||: |||: |||: |||: |||:  
 Db 344 PA-----NVDWMPATLAVIYVGGLITMCIDLGVSEYIROLHFFGRSLGRQFWMFTGGKV 397  
 R; Mortimore, B.  
 A; Reference number: Z19447  
 C; Accession: T21598  
 submitted to the EMBL Data Library, March 1997  
 A; Accession: T21598  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-443 <WIL>  
 A; Cross-references: EMBL:Z92832; PIDN: CAB07375.1; GSPDB: GN00023; CESP: F31D4.7  
 QY 274 AQASWWTGIVTARVTORGPSAPPEKEQPLPSSLP-----APPAVVEPAGR 322  
 A; Experimental source: clone F31D4  
 C; Genetics:  
 A; Gene: CESP-F31D4.7  
 A; Map position: 5  
 A; Introns: 13/3; 90/2; 149/1; 222/3; 290/3  
 Db 398 VHGEVFGVY-AFLQKNGLTA---EQTKLISQPEEVLIDCLINGRQPDLNWIGGR 451  
 QY 323 GSPRA--EKVTPSPPTASADYPSEN-----SDTOSERGCALPR--APR 371  
 A; Cross-references: EMBL:Z92832; PIDN: CAB07375.1; GSPDB: GN00023; CESP: F31D4.7  
 Db 452 YVPPDIIYFKWIHP----RTLSFASDRVLOSSMESLDLNTR-CSTARTLTPR 499  
 QY 9 LLAIVLVLVSGALVFOALEPQEQQAQ-----KKMDHGRQOFRLD 49  
 C; Species: Caenorhabditis elegans  
 C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999  
 C; Accession: T25392  
 R; Lloyd, C.  
 submitted to the EMBL Data Library, March 1997  
 A; Reference number: Z20027  
 A; Accession: T25392  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-393 <WIL>  
 A; Cross-references: EMBL:Z92813; PIDN: CAB07286.1; GSPDB: GN00021; CESP: T28A8.1  
 C; Genetics:  
 A; Experimental source: clone T28A8  
 A; Gene: CESP-T28A8.1  
 A; Map position: 3  
 A; Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2  
 Query Match 12.7%; Score 265; DB 2; Length 393;  
 Best Local Similarity 24.8%; Pred. No. 5.8e-10; DB 2;  
 Matches 77; Conservative 50; Mismatches 93; Indels 90; Gaps 8;  
 Amino acid sequence: -----HEQAQAKMDHGRDOFLRDPH 51  
 QY 7 ILLAALWLVLYUSGAWFOALEQ-----HEQAQAKMDHGRDOFLRDPH 51  
 ; |||: | :|||: |||: |||: |||:  
 Db 15 VSLIVLVSVYVYGFAGFLFYQLEQPNEVVRARNTERFRNIHKROMTEHLWEMRSGIGHV 74  
 C; Species: Caenorhabditis elegans  
 C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999  
 C; Accession: T24265  
 R; Wilkinson, J.  
 submitted to the EMBL Data Library, March 1996  
 A; Reference number: Z19866  
 A; Accession: T24265  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-522 <WIL>  
 A; Cross-references: EMBL:Z70036; PIDN: CAB093875.1; GSPDB: GN00028; CESP: T01B4.1  
 A; Experimental source: clone T01B4  
 C; Genetics:  
 A; Gene: CESP-T01B4.1  
 A; Map position: X  
 A; Introns: 95/3; 142/1; 224/3; 290/1; 458/1  
 Query Match 12.4%; Score 257; DB 2; Length 522;  
 Best Local Similarity 26.1%; Pred. No. 2.4e-09; DB 2;  
 Matches 79; Conservative 42; Mismatches 87; Indels 95; Gaps 10;

RESULT 11  
 T25392  
 hypothetical protein T28a8.1 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C; Accession: T25392  
 R; Lloyd, C.  
 submitted to the EMBL Data Library, March 1997  
 A; Reference number: Z20027  
 A; Accession: T25392  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-443 <WIL>  
 A; Cross-references: EMBL:Z92832; PIDN: CAB07375.1; GSPDB: GN00023; CESP: F31D4.7  
 A; Experimental source: clone F31D4  
 C; Genetics:  
 A; Gene: CESP-F31D4.7  
 A; Map position: 5  
 A; Introns: 13/3; 90/2; 149/1; 222/3; 290/3  
 Query Match 12.6%; Score 261.5; DB 2; Length 443;  
 Best Local Similarity 27.5%; Pred. No. 1.1e-09; DB 2;  
 Matches 84; Conservative 49; Mismatches 96; Indels 77; Gaps 10;  
 Amino acid sequence: -----KKNMDHGRQOFRLD 49  
 QY 9 LLAIVLVLVSGALVFOALEPQEQQAQ-----KKMDHGRQOFRLD 49  
 ; |||: | :|||: |||: |||: |||:  
 Db 17 LITVFLGQFVSGGLVFWLJEPYQSELDAWOKTIENNRTAVDAMMKLFFNSDLYI 76  
 C; Species: Caenorhabditis elegans  
 C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999  
 C; Accession: T24265  
 R; Wilkinson, J.  
 submitted to the EMBL Data Library, March 1996  
 A; Reference number: Z19866  
 A; Accession: T24265  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-522 <WIL>  
 A; Cross-references: EMBL:Z70036; PIDN: CAB093875.1; GSPDB: GN00028; CESP: T01B4.1  
 A; Experimental source: clone T01B4  
 C; Genetics:  
 A; Gene: CESP-T01B4.1  
 A; Map position: X  
 A; Introns: 95/3; 142/1; 224/3; 290/1; 458/1  
 Query Match 12.4%; Score 257; DB 2; Length 522;  
 Best Local Similarity 26.1%; Pred. No. 2.4e-09; DB 2;  
 Matches 79; Conservative 42; Mismatches 87; Indels 95; Gaps 10;

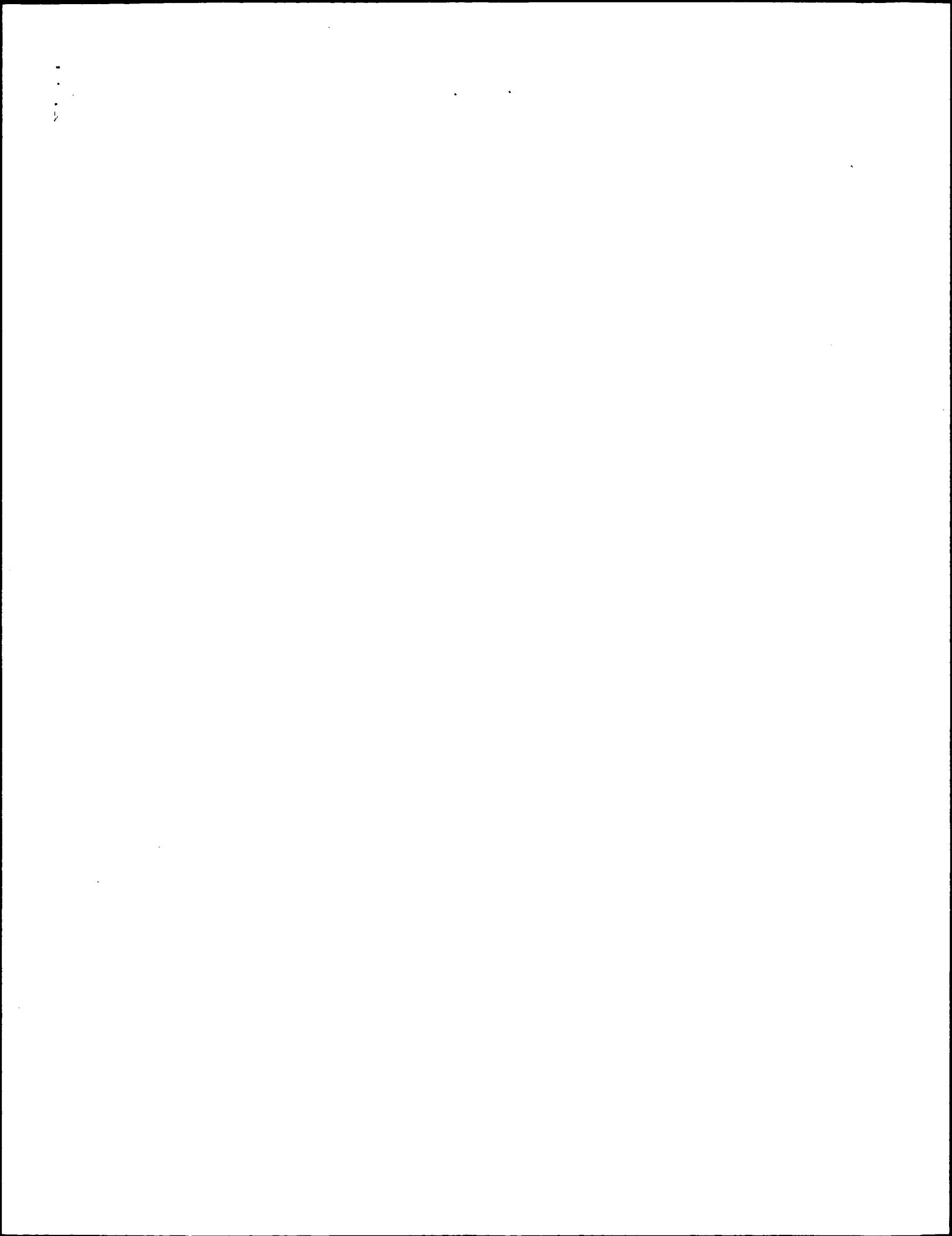
RESULT 13  
 T24265  
 hypothetical protein T01B4.1 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C; Accession: T24265  
 R; Wilkinson, J.  
 submitted to the EMBL Data Library, March 1996  
 A; Reference number: Z19866  
 A; Accession: T24265  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-522 <WIL>  
 A; Cross-references: EMBL:Z70036; PIDN: CAB093875.1; GSPDB: GN00028; CESP: T01B4.1  
 A; Experimental source: clone T01B4  
 C; Genetics:  
 A; Gene: CESP-T01B4.1  
 A; Map position: X  
 A; Introns: 95/3; 142/1; 224/3; 290/1; 458/1  
 Query Match 12.4%; Score 257; DB 2; Length 522;  
 Best Local Similarity 26.1%; Pred. No. 2.4e-09; DB 2;  
 Matches 79; Conservative 42; Mismatches 87; Indels 95; Gaps 10;

RESULT 12



Tue Jun 4 11:44:26 2002

us-09-655-272-2.rpr



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## Om protein - protein search, using sw model.

Run on: June 4, 2002, 11:00:36 ; Search time 31.9 Seconds  
(without alignments)  
2158.369 Million cell updates/sec

Title: US-09 655-272-2  
Perfect score: 2079  
Sequence: 1 MRSTILLALALVALVLYLVSG.....SKKPSRPRPGRLRDKAVPV 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:

562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_19;\*  
1: sp\_archaeal;\*  
2: sp\_bacteria;\*..  
3: sp\_fungi;\*  
4: sp\_invertebrate;\*  
5: sp\_mammal;\*  
6: sp\_micr;\*  
7: sp\_organelle;\*  
8: sp\_phage;\*  
9: sp\_plant;\*  
10: sp\_rabbit;\*  
11: sp\_rat;\*  
12: sp\_virus;\*  
13: sp\_vertebrate;\*  
14: sp\_unclassified;\*  
15: sp\_virus;\*  
16: sp\_bacteria;\*  
17: sp\_archeapl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID

Description

RESULT

ID

PREREQUISITE

PRTR:

419 AA.

096794

PRELIMINARY,

PRTR:

419 AA.

096794;

AC

01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT

01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE

TWO PORE K+ CHANNEL KT4.1B.

ID

CHNL

K+

CHANNEL

KT4.1B.

OS

Homo sapiens (Human).

OC

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX

NCBL\_TAXID=9606;

RN

[1]

SEQUENCE FROM N.A.

RA

Ozaita A., Vega-Saenz de Miera E.C.;

RT

\*Cloning of two transcripts of the Human 2-Pore K<sup>+</sup> channel KT4.1 Gene.

RT

Chromosomal Localization, Tissue Distribution and Functional

RT

Expression.;

RL

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

RL

EMBL; AR239501; AAC49390.1; -.

RP

KW

Ionic channel 419 AA; 45173 MW; E7BDE17B30C0FBF CRC64;

SQ

Query Match

Best Local Similarity

Score 81.4%;

Pred. No. 1692.5;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

Mismatches 41;

Score 81.4%;

Length 419;

DB 4;

Indels 5;

Gaps 2;

QY 181 CLIFLVLTPTFVFSYMSKLEAIFYVIVLTTVGFSDYVPGDGTSQNSPAPQPLWFWI 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 206 CLIFLVLTPTFVFCYMEDWSKLERIYFIVVLTITVGFDDYVAGADPRODSPAYQPLWFWI 265  
 QY 241 LFGLAYFASVLTIGNMLRVRAVERTRAEKGITAQASWTVTARVTORGPSARPEK 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 266 LGLGLAYFASVLTIGNMLRVRAVERTRAEKGITAQASWTVTARVTORGPSARPEK 325  
 QY 301 EQLLPSSPLPAWVTPAGRGSPAAEKETPSPATASALDYSENLADESSDTQS 360  
 ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 326 EQLL---LPPPCPAOLGRSPRSPEKQOPPSPTASALDYSENLADESSDTQS 381  
 QY 361 ERGCALPRAPRPRRRRNPKSKERSRPRGPGRLDEKAVPV 398  
 ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 382 ERGCALPRAPRPRRNPKVPRPGPGRFDKGVPV 419

RESULT 2  
 ID 092507 PRELIMINARY; PRT; 186 AA.  
 AC Q925Q7;  
 DT 01-DEC-2001 ('TREMBLrel. 19, Created)  
 DT 01-DEC-2001 ('TREMBLrel. 19, Last sequence update)  
 DR TWO\_PORE\_K+ CHANNEL\_KT4\_1 (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Ozaita A., Vega-Saenz de Miera E.C.;  
 RT "Cloning of Two Transcripts of the Human 2-Pore K<sup>+</sup> channel KT4.1 Gene.  
 RT Chromosomal Localization, Tissue Distribution and Functional  
 RT Expression.",  
 RL Submitted (APR 2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF239502; AAK49391.1; -.  
 KW IONIC CHANNEL.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 186 AA; 1982 MW; AB07DADBC867FFC7 CRC64;

Query Match 46.6%; Score 969; DB 11; Length 411;  
 Best Local Similarity 98.4%; Pred. No. 9.5e-50;  
 Matches 182; Conservative 1; Mismatches 57; Gaps 0;  
 Gaps 0;

QY 214 VFGSIVYPGDTGTSNPSAPQYQPLWFWILFLGLAYFASVLTIGNMLRAVSRRAREMGLT 273  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 2 VFGDGYVPGDGTGSNPSAPQYQPLWFWILFLGLAYFASVLTIGNMLRAVSRRAREMGLT 273

Db 274 AQASASWTGVTARYTQRGPSAPPEKEQPLPSSLAPPAPVVEPAGRGSPAPAEKET 333  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 62 AQASASWTGVTARYTQRGPSAPPEKEQPLPSSLAPPAPVVEPAGRGSPAPAEKET 121  
 QY 334 PSPTTASALDYPSENLAFTIDESSTQSERGCAALPAPRGRRRNPKSKPSRPGPGLRD 393  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 122 PSPTTASALDYPSENLAFTIDESSTQSERGCAALPAPRGRRRNPKSKPSRPGPGLRD 181  
 QY 394 KAVPV 398  
 |||||  
 Db 182 KAVPV 186

RESULT 3  
 ID 09NRT2 PRELIMINARY; PRT; 411 AA.  
 AC Q9NRT2;  
 DT 01-OCT-2000 ('TREMBLrel. 15, Created)  
 DT 01-OCT-2000 ('TREMBLrel. 15, Last sequence update)  
 DE TWO-PORE DOMAIN POTASSIUM CHANNEL\_TREK-1.

QY 181 CLIFLVLTPTFVFSYMSKLEAIFYVIVLTTVGFSDYVPGDGTSQNSPAPQPLWFWI 240  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 206 CLIFLVLTPTFVFCYMEDWSKLERIYFIVVLTITVGFDDYVAGADPRODSPAYQPLWFWI 265  
 QY 241 LFGLAYFASVLTIGNMLRVRAVERTRAEKGITAQASWTVTARVTORGPSARPEK 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 266 LGLGLAYFASVLTIGNMLRVRAVERTRAEKGITAQASWTVTARVTORGPSARPEK 325  
 QY 301 EQLLPSSPLPAWVTPAGRGSPAAEKETPSPATASALDYSENLADESSDTQS 360  
 ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 326 EQLL---LPPPCPAOLGRSPRSPEKQOPPSPTASALDYSENLADESSDTQS 381  
 QY 361 ERGCALPRAPRPRRRRNPKVPRPGPGRFDKGVPV 398  
 ||||| ||||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 382 ERGCALPRAPRPRRNPKVPRPGPGRFDKGVPV 419

RESULT 2  
 ID 092507 PRELIMINARY; PRT; 186 AA.  
 AC Q925Q7;  
 DT 01-DEC-2001 ('TREMBLrel. 19, Last annotation update)  
 DR TWO\_PORE\_K+ CHANNEL\_KT4\_1 (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,  
 RA Medhurst A.D., Murdoch P., Chapman C.G.;  
 RA Pfluegers Arch 439:714-722(2000).  
 DR EMBL: AF17106; ASN8943.1; -.  
 DR InterPro: IPRO03280; 2POREKCHANNEL.  
 DR InterPro: IPRO00636; Cation\_chan\_on\_lig.  
 DR InterPro: IPRO01622; Channel\_pore\_K.  
 DR Pfam: PF00520; ion\_trans; 1.  
 DR PRINTS: PRO1333; 2POREKCHANNEL.  
 DR PRINS; PRO1499; TREKCHANNEL.  
 KW Ionic channel;  
 SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;

Query Match 37.3%; Score 776.5; DB 4; Length 411;  
 best local similarity 49.8%; pred. no. 9.5e-50;  
 matches 142; conservative 57; mismatches 83; indels 3; gaps 1;

QY 1 MRSTLILLALLAVLVLYNSGALVFOALEQPHQOAKRMKDQHGDQFLRDPCVSOKSLED 60  
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 42 MRNKTVSPTFLVYLVLJGAVNFKALEQPHISQRTIVIQKQFQISQNCVNTELDE 101  
 QY 61 FIKLVLVERGGGANPETSWMUSSHSAWNNGSAFFSGTITGGYGNVLTHTDAGR 120  
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 102 LIQQIVAAANAGIIP--LGNISNQISHWDIGLSSFFFAGTVITIGFGNISPRTEGGK 158  
 QY 121 CIFVALVGIPLGFLGMLLAGVGDRLGSSLRRRGIGHIAIFLWVHPVPGLVLVLSAVFLIG 180  
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 159 CIYALIGIPLGFLLAGVGPOLGIIFGKGIAKVEDTFIWNVSOTKIRIISTIIFLIG 218  
 QY 181 CLIFLVLTPTFVFSYMSKLEAIFYVIVLTTVGFSDYVPGDGTSQNSPAPQPLWFWI 240  
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 219 CVLFVALPATIFKHKGWSALDAIVEWVITLTIGFDDYVAGGS DIEYLDPKVWFL 278  
 QY 241 LFGLAYFASVLTIGNMLRVRAVERTRAEKGITAQASWTVTARVTORGPSARPEK 285  
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 279 LVGLAYFAAVLMSMGDWLRVWISKKTEEVGEFRHAEAENPNTA 323

RESULT 4  
 ID 092414 PRELIMINARY; PRT; 370 AA.  
 AC Q92414;  
 DT 092414;  
 DT 01-DEC-2001 ('TREMBLrel. 19, created)  
 DT 01-DEC-2001 ('TREMBLrel. 19, last sequence update)  
 DE MECHANOSENSITIVE TANDEM PORE POTASSIUM CHANNEL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Kim Y., Bang H., Gratienco C., Kim D.;  
 RT "Synergistic interaction and the role of C-terminus in the activation  
 of TRAAK K<sup>+</sup> channels by pressure, free fatty acids and alkali";  
 RL Pfluegers Arch. 442:64-74(2001).  
 DR EMBL: AF202842; AAK60504.1; -.  
 KW Ionic channel.

SO	SEQUENCE	370 AA;	40874 MW;	54677E351CE64234 CRC64;
Query Match		37.0%	Score 768.5;	DB 11; Length 370;
Best Local Similarity	49.5%;	Pred. No. 3.9e-49;	DB 9;	Indels 3; Gaps 1;
Matches	141;	Conservative	57;	Mismatches 84;
QY	1	MRSTLALLALVLYLVLGALVFOALEQPHQQAOKKMDHQDFQLRDHPCVSOKSLED 60		
Db	42	MWKWVSTIFLFLVWLVLIGATVKALEQPOISORTIVIQONFIAQHACVNTELDE 101		
QY	61	FIKLIVEALGGGANPETSNTNSNHSSAWNLGSAGFFSGTITTYGYGNTVHTDAGRLF 120		
Db	102	LIOQIVTAINAGIIP--LGNNSNQVSHWDLGSSFFAGTIVTIGFNISPRTEGGKF 158		
QY	121	CIFYAALVGIPPLFGMLLAGYDRGSSLRKGIGHIEATFLKWHPPGLYRSLSAVFLIG 180		
Db	159	CIYALALGIPPLFGMLLAGYDOLGIFKGIAKEDTFIKWNQSQTKIRIISTILIFG 218		
QY	181	CULFVLTPTFVSYMESWSKLEAIYFVLTIVTUGFGDYVPGDGTGQNSPAYQPLWVMI 240		
Db	219	CVLFVALPAVIFKHIEGWSALDAIWFVLTITGFDYVAGGSDIEVLFYKEVWFWI 278		
QY	241	LFGLAYFASVLTIGNRLRAVSRTRAEMGLTAQASWGVFTA 285		
Db	279	LVGLAYFAVFLSMIGDWLRVLSKTTKEEVGEFRAHAAEWANTVA 323		
RESULT	5			
ID	Q92B6	PRELIMINARY;	PRT;	426 AA.
AC	Q92B6;			
DT	01-DEC-2001 (TREMBlre. 19, Created)			
DT	01-DEC-2001 (TREMBlre. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBlre. 19, Last annotation update)			
DE	2P DOMAIN POTASSIUM CHANNEL KCNK2.			
OS	Rat tus norvegicus (Rat);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
NCBI_TAXID	10116;			
RN	[1] SEQUENCE FROM N.A.			
RC	TISSUE="BRAIN";			
RX	MEDLINE=21219399; PubMed=11319556;			
RA	Bockenbauer D., Zilberman N., Goldstein S.A.;			
RT	"KCNK2": reversible conversion of a hippocampal potassium leak into a voltage-dependent channel. ";			
RT	Nat. Neurosci. 4:486-491(2001).			
RL	EMBL; AF325671; AAL01159.1; -.			
KW	Ionic channel;			
SEQUENCE	426 AA;	46912 MW;	CAICDA05BBE95FD8C CRC64;	
Query Match		37.0%	Score 768.5;	DB 11; Length 426;
Best Local Similarity	49.5%;	Pred. No. 3.9e-49;	DB 9;	Indels 3; Gaps 1;
Matches	141;	Conservative	57;	Mismatches 84;
QY	1	MRTTLLALLALVLYLVLGALVFOALEQPHQQAOKKMDHQDFQLRDHPCVSOKSLED 60		
Db	57	MKWTVSTIFLFLVWLVLIGATVKALEQPOISORTIVIQONFIAQHACVNTELDE 116		
QY	61	FIKLIVEALGGGANPETSNTNSNHSSAWNLGSAGFFSGTITTYGYGNTVHTDAGRLF 120		
Db	117	LIOQIVTAINAGIIP--LGNNSNQVSHWDLGSSFFAGTIVTIGFNISPRTEGGKF 173		
QY	121	CIFYAALVGIPPLFGMLLAGYDRGSSLRKGIGHIEATFLKWHPPGLYRSLSAVFLIG 180		
Db	174	CIYALALGIPPLFGMLLAGYDOLGIFKGIAKEDTFIKWNQSQTKIRIISTILIFG 233		
QY	181	CULFVLTPTFVSYMESWSKLEAIYFVLTIVTUGFGDYVPGDGTGQNSPAYQPLWVMI 240		
Db	234	CVLFVALPAVIFKHIEGWSALDAIWFVLTITGFDYVAGGSDIEVLFYKEVWFWI 293		
RESULT	6			
ID	Q96T55	PRELIMINARY;	PRT;	309 AA.
AC	Q96T55;			
DT	01-DEC-2001 (TREMBlre. 16, Created)			
DT	01-DEC-2001 (TREMBlre. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBlre. 16, Last annotation update)			
DE	2P DOMAIN POTASSIUM CHANNEL TALK-1.			
GN	KCNK16.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Cetaceans; Catarrhini; Hominidae; Homo.			
OX	NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G., Lazdunski M., Losage F.;			
RT	"Genomic and functional characteristics of novel human pancreatic domain K <sup>+</sup> channels.";			
RT	Biochem. Biophys. Res. Commun. 0:0-0(2001).			
RL	EMBL; AF358909; AAC49532.1; -.			
DR	MEAWYGVNPKNSTNPSN--WDFGSEFFAGTVWITGVGNLABSTEAGQFCVFA 129			
KW	Ionic channel;			
SEQUENCE	309 AA;	99C4B11EB26B0764 CRC64;		
Query Match		23.8%	Score 495.5;	DB 4; Length 309;
Best Local Similarity	37.2%;	Pred. No. 4.4e-29;	DB 4;	Indels 37; Gaps 9;
Matches	116;	Conservative	61;	Mismatches 98;
QY	6	LLAIALALVLYLVLGALVFOALEQPHQQAOKKMDHQDFQLRDHPCVSOKSLEDPIKLU 65		
Db	14	VLPILLAYVCLLIGATFQQLERQAEQSRDOPFOLKLRFENYQCDOMAMEQVQVI 73		
QY	66	VEAIGGAGPETSNTNSNHSSAWNLGSAGFFSGTITTYGYGNTVHTDAGRLCIFYA 125		
Db	74	MEAWYGVNPKNSTNPSN--WDFGSEFFAGTVWITGVGNLABSTEAGQFCVFA 129		
QY	126	LVGIPLEGMLLAGYDRGSSLRKGIGHIEATFLKWHVPP--GLVRSLSAVFLIGL 182		
Db	130	LIGIPLNVIFL--NHLGLGLRAHLAIE---RWEDRPRRSQSVLQYTLGLAFLFTGL 181		
QY	183	LFVLTVTPTFVSYMESWSKLEAIYFVLTIVTUGFGDYVPG-DCTGQNSPAYQPLWVMI 241		
Db	182	VLIPEPMWFSHVEGNSFSRGCFYPAITISTIGFDYVGTDSKHSVYRSLAJWIL 241		
QY	242	FGLAYFASVLTIGN-----WIRAVSRTRAEMGLTAQASW---TGTVTAFTV 288		
Db	242	LGIAALALIT-PIGLPLIHRCCQLWILSLRO-----GCGAKAAGRPPRRGSTAARGV 293		
QY	289	QRGPGSAPPK 300		
Db	294	QVTPDODPISKK 305		
RESULT	7			
ID	Q9H91	PRELIMINARY;	PRT;	294 AA.
AC	Q9H91;			
DT	01-MAR-2001 (TREMBlre. 16, Created)			
DT	01-MAR-2001 (TREMBlre. 16, Last sequence update)			
DT	01-OCT-2001 (TREMBlre. 18, Last annotation update)			
DE	DJ137F1.2. (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K).			
GN	DJ137F1.2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Cetaceans; Catarrhini; Hominidae; Homo.			
OX	[1]			

RP  
RA SEQUENCE FROM N.A.  
RL Williams S.;  
DR Submitted (SBR-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL: AL136087; CAC0736..1; -  
DR InterPro: IPR003280; 2pore channel.  
DR InterPro: IPR000336; Cation chan\_non\_lig.  
DR Pfam: PR00520; Channel\_pore\_K.  
DR PRINTS: PR01333; 2POREKCHANNEL.  
KW IONIC CHANNEL.  
SQ SEQUENCE 294 AA; 32507 MW; FCBA3B352F1E0952 CRC64;

Query Match 23.6%; Score 490; DB 4; Length 294;  
Best Local Similarity 40.8%; Pred. No. 1.1e-28;  
Matches 102; Conservative 54; Mismatches 78; Indels 16; Gaps 5;

QY 6 LLALLALVLVLYLVSGLVALQALEOPHEQQAQKKMDHGRDQFLRDHPVPSQKSLEDTIKL 65  
Db 14 VLPPLIAYCYLLGATIQQLERQAESQSDOFQLERLRFLENYTCDOWAMEQVQV 73  
QY 66 VEALGGGANPETSWNSSNHSSAVNLGSAFFSGTITTTIGGNIVHTDAGRIFCFYA 125  
Db 74 MEAWKGWVNPKGNSTNPSN--WDFGSSFFFRAGTVVTTIGYGNLAPSTEAGQCVFVA 129  
QY 126 LVGIPFLFGMLLAGVGDGRGSSLRGGHIEAFLKWHVPP--GLVRSLSLAVLFLLGCL 182  
Db 130 LGIPFLPLNIVFL---NHLGTGIRLAIE---RWEDEPERSQVQVQVGLALFLLGTL 181  
QY 183 LEVLTPTEVFSYMEWSNSKLEAYFVIVLTVGFGDVVPG-DGTOQNSPASYQPLMWIL 241  
Db 182 VILFPPMWFSHVEGWFSSEGYYFAFTLSTGFQDGVWVQDPSKHVISYRSLAIIWIL 241  
QY 242 FGLAYAFASVL 251  
Db 242 LGSLAWLALIL 251

RESULT 8

RP  
ID Q9BXD1 PRELIMINARY; PRT; 343 AA.  
AC Q9BXD1; DR 01-JUN-2001 (TREMBrel. 17, Created)  
DR 01-DEC-2001 (TREMBrel. 19, Last sequence update)  
DR POTASSIUM CHANNEL\_TASK-4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OK NCBI-TaxID=9606; RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=ADRENAL GLAND;  
RX MEDLINE=21145510; PubMed=11248242;  
RA Decher N., Maier M., Dittrich W., Gassnerhuber J., Bruggemann A.,  
RA Busch A.E., Steinmeyer K.;  
RT "Characterization of TASK-4, a novel member of the pH-sensitive, two-pore domain potassium channel family.",  
RT FEBs Lett. 432:84-89(2001);  
DR EMBL: AF339912; AAC2851..-  
DR InterPro: IPR003280; 2pore\_k\_channel.  
DR InterPro: IPR000656; Cation\_chan\_non\_lig.  
DR InterPro: IPR001622; Channel\_pore\_K.  
DR PRINTS: PR01333; 2POREKCHANNEL.  
SQ SEQUENCE 343 AA; 38172 MW; 29B1F354CE22E3BB CRC64;

Query Match 20.9%; Score 433.5; DB 4; Length 343;  
Best Local Similarity 36.2%; Pred. No. 1.9e-24;  
Matches 111; Conservative 49; Mismatches 120; Indels 27; Gaps 7;

QY 5 TLALLALVLVLYLVSGLVALQALEOPHEQQAQKKMDHGRDQFLRDHPVPSQKSLEDFIKL 64

Db 22 TWILLHA-YLAYLAIGTGFWTLEGRAACDSSRSFORQKWLQNFCQLDRPAFLDSLIR 80  
QY 65 LVEALGGGANPETSWNSSNHSSAVNLGSAFFSGTITTTIGGNIVHTDAGRIFCF 124  
Db 81 VVQAYKNGA---SLSNTSMGRWELVGSFFSVSTITIGGNLSPNTMARIICF 136  
QY 125 ALVGIPFLFGMLLAGVGDGRGSSLRGGHIEAFLKWHVPPGLVRSLSAVLFLLGCL 184  
Db 137 ALVGIPFLPLNIVFL---NRIGHLMQOGVNHMASRUGGTWQDPDKARNLAGSGALLSGLL 192  
QY 185 VLTPPFVFSMESNSKLEAYFVIVLTVGFGDVVPG-DGTOQNSPASYQPLMWIL 243  
Db 193 LLLPPLFESHMEGWSYTECFYFATITLUVGFGDVYVGMPSORYPLWKNMSLWIFG 252  
QY 244 LAYFASVLTTGNLRAVSRRT---PAMGCLTAQASWIGTVARVIO--TGPSADP 297  
Db 253 MA-----WALISNSSSPSWRQGGYVPAATTAAKRTSSPKAGRDITGSQSP 301  
Db 302 PHSKDAI 308

RESULT 9

RP  
ID Q96754 PRELIMINARY; PRT; 332 AA.  
AC Q96754; DR 01-DEC-2001 (TREMBrel. 19, Created)  
DR 01-DEC-2001 (TREMBrel. 19, Last sequence update)  
DE 2P DOMAIN POTASSIUM CHANNEL\_TALK-2.  
GN KNN17.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI-TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romeo G.,  
RA Lazdunski M., Le sage F.;  
RT "Genomic and functional characteristics of novel human pancreatic 2P domain K+ channels";  
RT Biochem. Biophys. Res. Commun. 0:0-0 (2001).  
DR EMBL: AF358910; AAC49533.1; -  
KW IONIC CHANNEL.  
SQ SEQUENCE 332 AA; 36894 MW; 1848DBC06E078158 CRC64;

Query Match 20.6%; Score 428.5; DB 4; Length 332;  
Best Local Similarity 36.0%; Pred. No. 4.4e-4;  
Matches 111; Conservative 49; Mismatches 115; Indels 33; Gaps 8;

QY 4 TTLLALLALVLVLYLVSGLVALQALEOPHEQQAQKKMDHGRDQFLRDHPVPSQKSLEDTIK 63  
Db 21 STVLLLA-YLAYLAIGTGFWTLEGRAACDSSRSFORQKWLQNFCQLDRPAFLDSLIR 79  
QY 64 LVEALGGGANPETSWNSSNHSSAVNLGSAFFSGTITTTIGGNIVHTDAGRIFCF 123  
Db 80 DVVOQAYKNGA---SLSNTSMGRWELVGSFFSVSTITIGGNLSPNTMARIICF 135  
QY 124 ALVGIPFLFGMLLAGVGDGRGSSLRGGHIEAFLKWHVPPGLVRSLSAVLFLLGCL 183  
Db 136 FALEVAFASVLTTGNLRAVSRRT---RTRAEMLGITAQASWIGTVARTQRGTPSA 295  
QY 184 VLTPPFVFSMESNSKLEAYFVIVLTVGFGDVVPG-DGTOQNSPASYQPLMWIL 242  
Db 192 PLLPLFISMEGWSYTECFYFATITLUVGFGDVYVGMPSORYPLWKNMSLWIFG 251  
QY 243 GLAYFASVLTTGNLRAVSRRT---RTRAEMLGITAQASWIGTVARTQRGTPSA 295  
Db 252 GMWALALITKLILSOLETPGRVCSCCHHSSKDF----KSQSW----RQGPDR 296

QY 295 PPPEKEQP 303  
Db 297 -EPESHSP 303

RESULT 10  
Q9JK62 PRELIMINARY; PRT; 5.02 AA.  
ID Q9JK62;  
AC 09JK62;  
DT 01-OCT-2000 (TREMBIrel. 15, Created)  
DE POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).  
GN KCNK5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TAXID=10090;  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=129/SVJ; TISSUE=KIDNEY;  
RA Roux J., Barhanin J.;  
RA "Mouse two p domain potassium channel TASK2.";  
RN Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2] SEQUENCE FROM N.A.  
RP TISSUE=KIDNEY;  
RA Cid L.P., Niemeyer M.I., Sepulveda F.V.;  
RT "Functional properties of mouse TASK-2 potassium channel.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
EMBL: AF29395; AAF88668.1; -;  
EMBL: AF319542; AG35056.1; -;  
DR MGI: MGI-1336175; KCNK5.  
DR InterPro: IPR003280; 2poreK-channel.  
DR InterPro: IPR00636; cation\_chan\_non\_lig.  
DR InterPro: IPR001622; Channel\_Pore\_K.  
DR PRINTS: PRO1333; 2poreKCHANNEL.  
KW IONIC CHANNEL 502 AA; 55976 MW; B4C7E7CC71B44D95 CRC64;

Query Match 20.3%; Score 421; DB 11; Length 502;  
Best Local Similarity 26.8%; Pred. No. 2.6e-23; Mismatches 129; Conservative 70; Gaps 20; Matches 147; Indels 136;

QY 9 LIAVLVLYLVSLVALVQALEQPHEDQAQKKMDHGRDQFLDRHPCVSOKSLEDITKLVLA 68  
Db 8 LSAAIFFYLAIGGAIKEFVLEBEEHHKEAKKNTYTKHLHLKEFPCLSQEGIDKLTQWVSDA 67

QY 69 LGGGANPETSWNNSNHSSAWNLGSAAFFSGTTTIGYNIIVLHTDAGRLFCITYALVG 128  
Db 68 ---ADCGVATIGNQTNN-WHWPNAMEFAATVITVITIGYGNVAPKTPAGRLFCYFYLGK 122

QY 129 IPL-----FQMLLAGYGDGRGSSL-RRGIG-----HEAIEFKWHVPPGLVRSLSAV 174  
Db 123 VPICLTWISALCKFFGGRAKRQLGFLTRRGYVSLRKAQITCTAFTIW----- 169

QY 175 LFLLIGLCLFLVLPPTFWFSYMSWSKLEAIIIVVILITVFGDVPGDGTQNSPA-YQ 233  
Db 170 ---GVVHLVHIPPFEMVTETWNYTEGLYSEFTITISTIGFGDFVAGVNPSANYHALYR 224

QY 234 PLWFWTLFLGFLAYFASVLTGIGWL-----RAYSRRTR-----AEMG 270  
Db 225 YFVELWIVYLGAW---LSLFNWKVSMFVEVHKAIKKRRRKESFESSHRSKALOMA 280

QY 271 GLTA-----QASWNGTV---TARVORTGSP-----PPEKEPLLP 306  
Db 281 GSTASKDNVIFLSLSKKEETYNDLIKQIGKKAMKTSGGGERVPGPGHGLGPQGDRLTIP 340

QY 307 SSLPAP-----PAVE-----PAG-RPGSPAPARKVET----- 333  
Db 341 ASL-APLVVYSKNRVPSLSEEVQTLKNKGHVRPLGEAGAOAKPSYQTSFVINQLDR 399

QY 334 -PSPPTASALDY----PSENLAFIGDESSDTQSERGCALPAPRGRRRPNSPKPSRPR 386  
Db 400 ISEREGPWEALDYHPLIFONANITFENE----ETGLSDEETSKSVDNLNTSKEQEQ 453

RESULT 11  
Q9CXB8 PRELIMINARY; PRT; 241 AA.  
ID Q9CXB8;  
AC 09CXB8;  
DT 01-JUN-2001 (TREMBIrel. 17, Created)  
DE POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).  
GN 3010005K4RIK PROTEIN.  
DE NCBI\_TAXID=10090;  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;  
RA MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda H., Kondo S., Yamamoto I.,  
RA Azawa K., Izawa M., Nishi M., Kyosava H., Kasukawa T., Saito R.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batyalov T., Casavant T.,  
RA Fleischmann R., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Sejia T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka R., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wernshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RA Hayashizaki I.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK019376; BAB31686.1; -;  
DR MGI: MGI-1924704; 3010005K4RIK.  
DR InterPro: IPR001622; Channel\_Pore\_K.  
SQ SEQUENCE 241 AA; 25796 MW; B4C39F77CD0A39DA CRC64;

Query Match 20.0%; Score 415.5; DB 11; Length 241;  
Best Local Similarity 46.1%; Pred. No. 2.8e-23; Mismatches 88; Conservative 32; Gaps 23; Indels 23; Gaps 4;  
Matches 88; Conservation 46.1%; Pred. No. 2.8e-23; Mismatches 48; Indels 23; Gaps 4;

QY 1 MRSTTLALLALVLYLVSLVALVQALEQPHEDQAQKKMDHGRDQFLDRHPCVSOKSLED 60  
Db 67 MKMKTTWAVLFWVVVWVYLTGGFLVRALEQPFESSOKNTIALEKAFRLDHICVSPOLET 126

QY 61 FIKLVLVEALGGGANPETSWNNSNHSSAWNLGSAAFFSGTTTIGYNIIVLHTDAGRLF 120  
Db 127 LIQHALDADNAGVSPV--GNNSNSHWDIGSAFFAGVITTYGYNAPSPEGK 183

QY 121 CTFVALGVPRLMLLAGVDFGSSLRRGIGHIAFLKWHVPPGLVRSLSAVFLIG 180

Db 184 CILKAIFGGLPLFGFLLAGIJDOLGTIFGKSTARVERVF-RAH-----G 225

QY 181 CLLFVLTPTFV 191  
Db 226 C-FVCTHIFV 234

RESULT 12  
 Q9ERU5 PRELIMINARY; PRT; 313 AA.  
 ID Q9ERU5; PRELIMINARY; PRT; 313 AA.  
 AC Q9ERU5;  
 DT 01-MAR-2001 (TREMBREL 16, Created)  
 DT 01-MAR-2001 (TREMBREL 16, Last sequence update)  
 DT 01-OCT-2001 (TREMBREL 18, Last annotation update)  
 DE 2P DOMAIN K+ CHANNEL TWIK-2.  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX NCBI\_TAXID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=SPRAGUE-DWYLEY;  
 RA MEDLINE=20435832; PubMed=10887187;  
 Patel A.J., Maincret F., Magnone V., Fosset M., Lazdunski M.,  
 Honore E.; "TWIK-2, an inactivating 2P domain K<sup>+</sup> channel.";  
 RL J. Biol. Chem. 275:28722-28730(2000).  
 DR EMBL; AR281304; RAGI0508; 1; -.  
 DR InterPro; IPR003280; 2POREK\_channel.  
 DR InterPro; IPR00636; Cation\_chan\_non\_lig.  
 DR InterPro; IPR00636; Channel\_pore\_K.  
 DR InterPro; IPR001179; TWIK1\_channel.  
 DR Pfam; PF00520; ion\_trans\_1.  
 DR PRINTS; PRO1333; 2POREK\_CHANNEL.  
 DR PRINTS; PRO1096; TWIK1\_CHANNEL.  
 DR PRINTS; PRO1096; 2POREK\_CHANNEL.  
 KW Ion channel; TWIK CHANNEL.  
 SQ SEQUENCE 313 AA; 38228 MW; 5E78031947D75DE6 CRC64;

Query Match 18.8%; Score 390; DB 11; Length 313;  
 Best Local Similarity 35.1%; Pred. No. 2.9e-21; Gaps 8;  
 Matches 98; Conservative 50; Mismatches 101; Indels 30; Gaps 8;

Qy 8 ALLALVIL---YLVSGLYFQALEQPHEOQAOKMDHGRDQFLRDHPCVQSLED 63  
 Db 5 ALLASALVALVAGYLAGLALVLRPHEARLRAELGTUREQLRLRHSPCVAAHALDAFVE 64  
 Qy 64 LLVEA-----LGGGANPETSWTNNSNNISAWNLGSAFFFSMIIITGYYGNVLHDA 116  
 Db 65 RVALAAGRIGRIGLAVLANASGP---ANASD -PAWDFASALAFFAVLTIVTGYTPLRDA 118  
 Qy 117 GRFLCIFYALVGIPLFGMILLAGVGDRLSSLRSGTGHIEAIFLKWHVPGVGLVSLSAVLE 176  
 Db 119 GKAFTSIVFALLGVPTMLLTTASAQRLL--SLLTHAPLWSLWRGWHPORAARWHLVAL 176  
 Qy 177 LLIGCLLFVLTPTPEVFSYM-ESMSKLEAYFVIVLTIVFGFGIVYPGDTGQ-NSPAVQP 234  
 Db 177 LMVIVAAFLIPAAVFAVYLEAWSFLDAFYFCISLSTIGLSDYVPGEAFCGPYRSLYKV 236  
 Qy 235 LWVWILFGLAVFAVSLTIGNMLRAVSRTRAREMGLT 273  
 Db 237 LVTAVLFLGLSVAVMLVLOP-----RRVSDLHLGT 266

RESULT 14  
 Q99L99 PRELIMINARY; PRT; 336 AA.  
 ID Q99L99; PRELIMINARY; PRT; 336 AA.  
 AC Q99L99;  
 DT 01-JUN-2001 (TREMBREL 17, Created)  
 DT 01-DEC-2001 (TREMBREL 19, Last sequence update)  
 DE POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 1.  
 GN KCNK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 DR Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC00329; AAH03729; 1; -.  
 DR MGD; MGI:109322; KCNK1.  
 DR InterPro; IPR00636; 2POREK\_Channel.  
 DR InterPro; IPR00636; Cation Chan Non Lig.  
 DR InterPro; IPR001622; Channel\_pore\_K.  
 DR Pfam; PF00520; ion\_trans\_1.  
 DR PRINTS; PRO1333; 2POREK\_CHANNEL.  
 DR PRINTS; PRO1096; TWIK1\_CHANNEL.  
 SQ SEQUENCE 336 AA; 38201 MW; 76B7FD5361A6216C CRC64;

Query Match 18.1%; Score 376.5; DB 11; Length 336;  
 Best Local Similarity 34.4%; Pred. No. 3.2e-20; Gaps 9;  
 Matches 90; Conservative 53; Mismatches 96; Indels 23; Gaps 9;

RN [1]  
 RA SEQUENCE FROM N.A.  
 RN NCBL\_TAXID=10116;  
 RN [1]  
 RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,  
 RA

QY 2 RSTILLALAL-VILLYLVSGLATVQAOLEPHEQAOAKMDHGKDFQFLRDHPCVSOKSLIED 60  
 Db 18 RSMACFGFLVLYLVLVFGAVVFSVELPYEDLROLRKLRFLFEECLSEPOLEQ 77  
 QY 61 FIKLVEALGGG---ANPETSWNSSHHSSAANLGSAAFFSCTIITIGYCNIVHTDA 116  
 Db 78 FLGRVLEASNYGVSVLSNASGNNN-----WDFTSALFFASTVLSITGYGHVPLSDG 129  
 QY 117 GRLCIFVALVGIPFLGMLLAGVGDRLGSSL-PRRGIGHIEATFLKWHVPPGLVRSLSAVL 175  
 Db 130 GKACCIISVIGIPFTLFTAVQRVTVHYTRPVYFH---IRMGPSKQVAVIHWAVL 186  
 QY 176 --FLLIGCLLFVLTPTFVFSYME-SWSKLEATVFVIVLTVFGDXVPGDGTGQN-SPA 231  
 Db 187 LGFTIVSCFFI-PAAEVSVDWDNFILESYFCFISLSTIGLGDIVPGEGINQKREL 244  
 QY 232 YQPLVWFLFGLAYFASVLT 233  
 Db 245 YKIGTCYLLGLIAMLVLET 266

RESULT 15  
 Q9H592 PRELIMINARY; PRT: 229 AA.  
 ID Q9H592;  
 AC 09H592;  
 DT 01-MAR-2001 (TREMBUREL, 16, Created)  
 DT 01-MAR-2001 (TREMBUREL, 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBUREL, 17, Last annotation update)  
 DE DJ137F1.1 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SURFAMILY K )  
 DE (FRAGMENT).  
 GN DJ137F1.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Williams S.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/PDBJ databases.  
 DR EMBL: ALI3607; CAC07335.1;  
 DR InterPro: IPR001622; Channel\_pore\_K.  
 DR PRINTS: PRO1333; 2POREKCHANNEL.  
 KW Ionic channel.  
 FT NON\_TER 229  
 SQ SEQUENCE 229 AA: 25344 MW: TAB9FB847F242ECE CRC64:

Query Match 17.8%; Score 370.5; DB 4; Length 229;  
 Best Local Similarity 40.6%; Pred. No. 5.6e-20; Gaps 3;  
 Matches 88; Conservative 37; Mismatches 83; Indels 9;

QY 4 TTIALLALLAVLVLIVSGALVFOQLEPHEQQAKKMDHGRDOFLRDHPCVSOKSLDFIK 63  
 Db 21 STVILLLA-YLVAYALGIGVFWTLEGRAAQDSSRSFORDKWEILQNFTCIDRPALDSLIR 79  
 QY 64 LVEALSGGANPNTSWNSNSHSAWNGSARFFSGITITIGYGNVLHDAIGRCIF 123  
 Db 80 DVOQAYKNGA---SLLNTTSNGRWEVGSIFPSVTITIGYGNLSPNTMARIFCIF 135  
 QY 124 YAVGICPLEGMLLAGVDRGLGSSLRGIGHTEAIFLKWHVPPGLVRSLSAVLFLIGCLL 183  
 Db 136 FAIVGIPNLNVWL---NRLGHMOCVNHWASRLEGQTWQDPDKARWLAGSGALUSGLL 191  
 QY 184 FVIGTPFWFSYMSWSKLEATIVVIVLTVFGDYV 220  
 Db 192 FILLPLPLFSHMGWSTIEGFYFAFITLSTVFGDYV 228

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